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                                        CAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAGAT
                                                                         1146 AGCCAATCTGATCCCAGGGTTGAACCTCAGCGCACTTGGCATCTTTTCAACAGGACTGTC
                              AATTGAACATGAAACAGGGACCAAGATAAACAATCTCATCTTTGCAGGATTTGAGCATATA
                                                                                              CGTGCTATCTCCACCAGGGCCCCGGGAGCTCCCCCGGTGCCCCTACCACCACTT
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; Sequence 749, Application US/09764864
; Patent No. US20020132783A1
; GBNERAL INFORMATION:
; APPLICANT: Rosen et al.
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                                                                                              41.7%; Score 1423.8; J
88.4%; Pred. No. 0;
ive 0; Mismatches
              0.1
NUMBER OF SEQ ID NOS: 133
SOFTWARE: CuraSeqList version 0...
SOFTWARE: CuraSeqList version 0...
LENGTH: 1707
TYPE: DNA
ORGANISM: Homo sapiens
FATURE:
NAME/KEY: CDS
JOCATION: (5)..(1669)
US-10-262-445-39
                                                                                                                Conservative
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683 AGGGGCCGAGGAGGGGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGAGCCCCGCCT
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Sequence 330, Application US/09764864

Batent No. US20020132753A1

GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBNE: PTZ3

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrappe
NUMBER OF SEQ ID NOS: 1792

SOFTWARE: Patentin Ver. 2.0
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LOCATION: (441)
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US-09-764-864-330
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Pred. No. 1.4e-290;
3; Mismatches 12;
              and
                                                             Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 1792 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 749
            TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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NAME/KEY: SITE
LOCATION: (774A)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
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Best Local Similarity 98.4%;
Matches 1145; Conservative
                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
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LOCATION: (511
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; TYPE: DNA
; ORGANISM: HOMO S
US-09-735-705-347
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Sequence 347, Application US/09735705

Sequence 347, Application US/09735705

Setent No. US2002005232941

APPLICANT: Wang, Tongtong

APPLICANT: Ralos, Michael D.

APPLICANT: Bosken, Nancy

APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Wang, Ahjun

APPLICANT: Whell, Patricia D.

APPLICANT: Ranger, Neil

APPLICANT: Composition of Applicant Ranger, Neil

TITLE OF INVENTION: Composition D.

CURRENT APPLICATION OF SECULATION COMPOSITIONS AND METHODS FOR THE THER FILLE REFERENCE: 210121.455C14

CURRENT APPLICATION OF SECULATION COMPOSITIONS OF LUNG CANCER

CURRENT FILLE REFERENCE: 210121.455C14

CURRENT APPLICATION COMPOSITIONS OF LUNG CANCER

CURRENT FILLE REFERENCE: 2000-12-12

NUMBER OF SEQ ID NOS: 419
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                                                                                                                    81;
                                                                                   Length 1740;
                                                                                                                      Indels
                                                                                   Score 712; DB 9; Lt
Pred. No. 1.8e-184;
0; Mismatches 555;
                                                                                      Query Match 20.9%;
Best Local Similarity 64.5%;
Matches 1156; Conservative
                                               sapiens
SEQ ID NO 347
LENGTH: 1740
TYPE: DNA
ORGANISM: HOMO 5
                                                            US-09-850-716A-347
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Sequence 347, Application US/09850716A
Sequence 347, Application US/09850716A
Sexemin No. US20020115139A1
GENERAL INFORMATION:
APPLICANT: Modeil, Patricia D.
APPLICANT: Retter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C15
CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 3.0
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CANCER

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FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 347
 AND DIAGNOSIS OF
                                                                                                                                  Query Match 20.9%;
Best Local Similarity 64.5%;
Matches 1156; Conservative (
                                                                                     TYPE: DNA
CRGANISM: Homo sapiens
US-09-897-778-347
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                                       81;
     Length 1740;
                                      Indels
Score 712; DB 9; L. Pred. No. 1.8e-184; 0; Mismatches 555;
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Fanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

Sequence 347, Application US/09897778 Patent No. US20020147143A1 GENERAL INFORMATION:

-09-897-778-347

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Sequence 347, Application US/10007700 Publication No. US20030064947A1 GENERAL INFORMATION:
APPLICANT: Wang, Tongtong APPLICANT: Wang, Aijun APPLICANT: Skeiky, Yasir A.W. APPLICANT: Li, Samual X.

SULT 14 -10-007-700-347

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                     APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Neil.
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APPLICANT: Carter, Darrick
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APPLICANT: Cai, Feng W.
APPLICANT: Cai, Feng M.
APPLICANT: Poy, Teresa M.
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Pred. No. 1.8e-184;
0; Mismatches 555;
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Kalos, Michael D.
Henderson, Robert
McNeill, Patricia
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CORGANISM: Homo sapiens
US-10-007-700-347
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Best Local Simi:
Matches 1156;
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Application US/10117982
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APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Garter, Darrick
APPLICANT: Handerson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Maricle, Barbara
APPLICANT: Spies, Gregory A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.9%;
Best Local Similarity 64.5%;
Matches 1156; Conservative
                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Matcale, Michael D.
APPLICANT: Marcicle, Barbara
APPLICANT: Spies, Gregory A.
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Wang, Tongtong
ITLLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
ITLLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/10/117,982
UUMBER OF SEQ ID NOS: 484
SOFTWARE: RASTSEQ for Windows Version 4.0
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Pred. No. 1.8e-184;
0; Mismatches 555;
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541 AGGENGGGGLICCAGGATTGTTGCTGCCATCATCGGAAAGGAGGCCTTGACCATAAAGAAC 723 664 CTGGTCCCCACCAGTTTGTTGGTGCCATCATCGGAAAGGAGGCCTTGACCATAAAGAAC 723 601 CTGGTTCCCACCAATTGTTGGAGCCATCATAGGAAAGAAGGAGGCCACCATTCGGAAC 660
724 ATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGACTCTGGAGCTGCA 783 
784 GAGAAGCCTGTCACCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGAIT 843 
844 CTTGAAATCATGCAGAAAGGGGGAGATGAGCCAAACTAGCCGAAGAGATTCCTCTGAAA 903 
904 ATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGCAGAAATTTGAAG 963 
964 AAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATA 1023
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1084 ATAGRGATTARGAAGAGCTGCGTGAGGCCTTTGAAAATGATAGCTGGCTGTTAACCAA 1143 1021 GAGGAGATCATGAAGAAAATCAGGGAGTCTTATGAAAATGATATTGCTTCTATGAATCTT 1080
1144 CARGCCARICTGATCCCAGGGTTGAACCTCAGCGCACTTGGCATCTTTCAACAGGACTG 1203 
1204 TCCGTGCTATCTCCACCAGGAGGGCCCGGGAGCTCCCCCGCTGCCCCTACCACCCC 1263
1264   TTCACTACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGGTTTGGCCGGTTC   1323
1324 CCGCATCATCACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCT 1383 
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1564 GAAAACTTCTTTAACCCAAAGAAGAGAGAGGCGAAGCGCATATCAGAGTGCCTCT 1623 
1624 TCCACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC

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- protein search, using frame\_plus\_n2p model

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July 16, 2004, 11:17:53

US-09-270-437D-6

1120

Perfect score:

Sequence:

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Pypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
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C;Species: Protein T57420
R;White, O.; Risen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Recession: F75420
A;Recellecule type: DNA
A;Residues: 1-319 eWHI>
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MDBL=frame+ n2p.model -DEV=xlp
Q=(cgn2_1/05F0^{o} spool_pVUS09270437/runat_16072004_113128_13969/app_query.fasta_1.3591
-Q=(cgn2_1/05F0^{o} spool_pVUS09270437/runat_16072004_113128_13969/app_query.fasta_1.3591
-DB=PIR_78 -OFMATERX=0190.rpr -MINRATCH=0.1 -LOOPEXT=0
-UNITS=Eits -START=1 -END=-1 -MATRIX=01190 -TRANS=human40.cdi -LIST=45
-UNITS=Eits -START=1 -END=-1 -MATRIX=01190 -TRANS=human40.cdi -LIST=45
-NORM=ext -HERPSIZE=500 -MINIEN*0 -MAZIEN=20000000000
-USER=US09270437_@CGN 1 1 86 @runat 16072004 113128 113969 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=IO0 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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SUMMARIES

\_pirl:\* pir2:\* pir3:\*

PIR\_78:\*

Database

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Result М М AB1422 AB1422 AB1796 WZBEN3 JC7957 T29850 FGHUB

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S52099 173957 TVHURS T12121

2338 2347 63

JS0747 T49915 A29635

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Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries

seq length: 0 seq length: 200000000

Minimum DB Maximum DB

segs, 96191526 residues

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Searched:

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procein-serine/threonine kinase (EC 2.7.1.-) - suid herpesvirus 1 (strain NIA-3) protein NyAlternate names: UL13 protein (EC 2.7.1.-) - suid herpesvirus 1 (strain NIA-3) NyAlternate names: UL13 protein (S.Species: suid herpesvirus 1 (S.Species: suid herpesvirus 1 (S.Species: al-1993 #sequence_revision 30-Jun-1993 #text_change 11-Jun-1999 (S.Speciesion: B4274 Ride Wind, N.; Domen, J.; Berns, A. J. Virol. 66, 5200-5209, 1992 A; Pittle: Herpesviruses encode an unusual protein-serine/threonine kinase which is nones A; Accession: B42744 MUD:92365105; PMID:1323689 A; Accession: B42744 A; MoulD:92365105; PMID:1323689 A; Mesidues: 1-398 GBEN>AA47481.1; PID:9334094 A; Cross-references: GB:M94870; NID:9334092; PIDN:AAA47481.1; PID:9334094 A; Cross-references: GB:M94870; NID:9334092; PIDN:AAA47481.1; PID:9334094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sex-determining region Y (SRY)-like HMG-box protein 17, SOX17 protein - rice field eel C; Species: Monopterus albus (rice field eel)
C; Species: Monopterus albus (rice field eel)
C; Date: 22-Jun-2003 #sequence_revision 22-Jun-2003 #text_change 07-Jul-2003
C; Accession: UC7957
R; Wang, R.; Cheng, H.; Xia, L.; Guo, Y.; Huang, X.; Zhou, R.
Biochem. Biophys. Res. Commun. 303, 452-457, 2003
A; Title: Molecular cloning and expression of Sox17 in gonads during sex reveral in the A; Reference number: UC7957; MUID:22546426; PMID:12659838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-39 sWAN>
Zross-treferences: GB:AY100695
C;Comment: This protein functions as a transcriptional activator during spermatogenesi
C;Comment: This protein functions
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C,Keywords: gonad differentiation; HMG box; sexual differentiation; Sox17; spermatogen
                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: ULJ3
C;Superfamily: herpesvirus protein-serine/threonine kinase; protein kinase homology
C;Superfamily: phosphotransferase; serine/threonine-specific protein kinase
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;78-378/Domain: protein kinase homology <KIN>
F;86-93/Region: protein kinase ATP-binding motif
F;86-93/Region: protein kinase ATP-binding F;103/Active site: Lys #status predicted
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probable GTP-binding protein homolog lmo2779 [imported] - Listeria monocytogenes (strain C; Species: Listeria monocytogenes C; Species: Listeria monocytogenes C; Species: Listeria monocytogenes C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C; Accession: AB1422
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker S; Glaser, P.; Frangeul, L.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Sainoes, L.M.; Karst, U. Sainoes, L.M.; Karst, U. Sainoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, O.; Schlueter, T.; Sainoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Reference number: AB1077; MulD:21537279; PMID:11679669
A; Residues: Dreliminary
A; Molecule type: DNA
A; Residues: 1.366 cGLA>
A; Residues: 1.366 cGLA>
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A; Residues: 1.366 cGLA>
A; Residues: 1.366 cGLA>
A; Residues: 1.366 cGLA>
A; Cross-references: GB:NC_003210; PIDN:CAD00992.1; PID:gl6412279; GSPDB:GN00177
A; Genetics:
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A,Experimental source: strain Clip11262
C;Genetics:
A,Gene: lin2919
C;Superfamily: yeast probable purine nucleotide-binding protein YBR025c
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C,Superfamily: yeast probable purine nucleotide-binding protein YBR025c
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A;Residues: 1-366 <GLA>
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A; Molecule type: protein
R; Masidues: 31-112, Ev. 114-137, QS', 140-144, QP', 147-148 <BLO>
R; Masidues: 31-112, Ev. 114-137, QS', 140-144, QP', 147-148 <BLO>
R; Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.
Biochemistry 33, 1988-1993, 1994
Biochemistry 33, 1988-1993, 1994
A; Title: Identification of proteins associated with apolipoprotein A-I-containing lipopr A; Reference number: A54223; MUID:94162201; PMID:8117655
A; Accession: G54223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A;Title: Covalent structure of fibringen.
A;Reference number: A90037; MUID:82254370; PMID:6575689
A;Contents: annotation; review, disulfide bonds
A;Contents: annotation; review, disulfide bonds
Bir. J. Biochem. 77, 595-610, 1977
A;Title: Primary structure of human fibrinogen. Characterization of disulfide-containing
A;Reference number: A91249; MUID:77245999; PMID:891553
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A;Contents: annotation; review, EM structure, polymerization, ligands
A;Contents: annotation; review, EM structure, polymerization, ligands
A;Chung, D.W.; Rixon, MW.; Que, B.G.; Davie, B.W.
Ann. N. Y. Acad. Sci. 408, 449-456, 1983
A;Fitle: Cloning of fibrinogen genes and their cDNA.
A;Reference number: A90038; MUID:83254384; PMID:6575700
B;Kirschbaum, N.E.; Budzynski, A.Z.
G. Biol. Chem. 265, 13669-13676, 1990
A;Contents: annotation
B;Kirschbaum, N.E.; Endzynski, A.Z.
A;Contents: annotation; hementin cleavage site
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A;Introns: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:FC
ins are contained in the core. Two three-chain coiled coils emerge from this core and cc
from the distal domain nodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Contents: annotation; disulfide bonds
Kboolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Cassman, K.G.; (
in Regulatory Proteclytic Enzymes and Their Inhibitors, Magnusson, S., Ottesen, M., Folt
A; Title: The structures of fibrinogen and fibrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Note: hementin, a protease from Haemereria ghilianii, the giant South American leech, C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave C;Comment: The soponsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein
A;Residues: 31-144, QF',147-231,'D',233-330,'E',332-491 <WAT>
R;Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A;Reference number: A94309; MUID:76225080; PMID:936108
                                                                                                                                                                                                                                                      A;Title: Amino acid sequence of the beta chain of human fibrinogen. A;Reference number: A90437; MUID:79124640; PMID:420779
                                                                                                     A;Molecule type: protein
A;Residues: 31-137, QS',140-144, QF',147-491 <HEN>
R;Matt, K.W.K.; Takagi, T.; Doolittle, R.F.
Biochemistry 18, 68-76, 1979
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A)Cross-references: GDB:119130; OMIM:134830
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A;Contents: annotation; disulfide bonds
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Annu. Rev. Biochem. 53, 195-229, 1984
A;Title: Fibrinogen and fibrin.
                               A; Contents: carbohydrate binding
A; Reference number: A94433
                                                                                                                                                                                                                                                                                                                                         A; Accession: A90437
                                                                      A; Accession: A94433
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N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide B
C;Species: Homo sapiens (man)
C;Date: 24-Apr.1984 #sequence revision 31-Mar.1993 #text change 08-Dec-2000
C;Accession: B43568; A90469; E30469; I37389; A94433; A90437; A94309; G54223; A03121; B37
R;Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A;Reference number: A43568; MUID:91344740; PMID:2102623
A;Accession: B43568
A;Molecule type: DNA
A;Residues: 9-191, 'p', 193-491 < CHU>
R;Chung, D.W.; Que, B.G.; Rixon, M.W.; Mace Jr., M.; Davie, E.W.
Biochemistry 22, 3244-3250, 1983
A;Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonu
A;Reference number: A90469; MUID:83283433; PMID:6688356
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A;Rolecule type: DNA
A;Residues: 1-38 < HUB>
A;Cross-retences: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
A;Cross-retences: EMBL:X05018; NID:g31400; PIDN:CAA28674.1; PID:g31401
B;Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, B.
in Protides of the Biological Fluids, Proc. 28th Collog., Peeters, H., ed., pp.51-56, Pe
A;Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
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A; Residues: 1-38 <CH1>
A; Residues: 1-38 <CH1>
A; Rocession: B90469
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 9-191, 'A', 193-491 <CH2>
A; Cross-references: GB:000129; NID:g182429; PIDN:AAA52429.1; PID:g182430
B; Huber, P.; Dalmon, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
A; Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
A; Reference number: 137389; MUID:87146483; PMID:3029722
           hypothetical protein (49C8.5 - Caenorhabditis elegans
C,9Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C,Accession: T29850
R,Johnson, D.; Bradshaw, H.
Submitted to the BMBL Data Library, June 1996
A,Pescription: The sequence of C. elegans cosmid (49C8.
A,Reference number: 220698
A,Accession: T29850
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule Lype: DNA
A,Molecule Lype: DNA
A,Residues: 1-431 <-JOH>
A,Residues: 1-431 <-JOH>
A,Residues: 1-431 <-JOH>
A,Resperimental source: EMBL:UG1945; PIDN:AAB03126.1; GSPDB:GN00022; CESP:C49C8.5
A,Gene: CESP:C49C8.5
A,Gene: CESP:C49C8.5
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A,Introns: 17/3; 66/2; 106/3; 151/2; 187/1; 233/2; 302/3; 329/1; 351/2; 377/2
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us-09-270-437d-6.0ligo.rpr

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C;Špecies: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 01-Dec-2000
C;Accession: 350747; S25287
Aimataka, H.; Sogawa, K.; Yasumoto, K.; Kikuchi, Y.; Sasano, K.; Kobayashi, A.; Hayamı
submitted to JTPID, September 1992
A;Reference number: JS0747
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A.Molecule type: mRNA
A.Molecule type: mRNA
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A.Molecule type: mRNA
A.Kossidues: 1-788 <IMA>
A.Crossidues: 1-788 <IMA>
A.Crossidues: 1-1788 <IMA>
A.Crossidues: 1-128 <IMA>
A.Crossidues: 1-128 <IMA>
A.Crossidues: 1-128 <IMA>
A.Crossidues: 1-122 <IMA
A.Molecule type: mRNA
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NyAlternate names: protein T24H18.180

Syspecies: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-uun-2000 #sequence_revision 02-uun-2000 #text_change 02-uun-2000

C;Accession: T49915

E;Bevan, M.; Robben, J.; Grymonprez, B.; Volckaert, G.; Bancroft, I.; Mewes, H.W.; Rudcherence number: Z25024

A;Reference number: Z25024

A;Accession: T49915
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A;Molecule type: DNA
A;Residues: 1-1226 <BEV>
A;Cross-references: BMBL:AL353013; GSPDB:GN00063; ATSP:T24H18.180
A;Experimental source: cultivar Columbia; BAC clone T24H18
C;Genetics:
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A;Introns: 2/3; 40/1; 111/1; 123/3; 183/3; 231/1;
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                                                                      US-09-270-437D-6 (1-3412) x A29635 (1-696)
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A; Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into A; Pathway: blood coagulation
C; Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfic C; Superfamily: fibrinogen beta chain; fibrinogen beta setatus predicted csig.
C; Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglutamic ac; F;1-30/Domain: (or 4-30 or 15-30) signal sequence #status predicted csig.
F;31-44/Product: fibrinogen beta chain #status experimental cAPT>
F;45-41/Product: fibrinogen beta chain #status experimental cAPT>
F;45-41/Product: fibrinogen disulfide ring homology cFBG>
F;38-48/Poomain: fibrinogen disulfide ring homology cFBG>
F;38-48/Poomain: fibrinogen disulfide ring homology cFBG>
F;38-48/Poomain: fibrinogen disulfide ring homology cFBG>
F;38-48/Poomain: fibrinogen disulfide ring homology cFBG>
F;38-48/Poomain: fibrinogen beta/gamma homology cFBG>
F;38-48/Poomain: fibrinogen disulfide ring homology cFBG>
F;38-48/Poomain: fibrinogen (to alpha-55) #status experimental
F;44-45/Cleavage site: Arg-d1y (thrombin) #status experimental
F;55/Disulfide bonds: interchain (to alpha-68) #status experimental
F;237/Disulfide bonds: interchain (to alpha-184) #status experimental
F;237/Disulfide bonds: interchain (to alpha-184) #status experimental
F;237/Disulfide bonds: interchain (to alpha-184) #status experimental
F;237/Disulfide bonds: interchain (to alpha-184) #status experimental
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F;237/Disulfide bonds: interchain (to alpha-184) #status experimental
F;237/Disulfide bonds: interchain (to alpha-184) #status experimental
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NyAlternate names: finger protein ZNF76
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Accession: A29635; G44256
R.Kadonaga, J.T.; Carner, K.R.; Masiarz, F.R.; Tjian, R.
Cell 51, 1079-1090, 1987
A.Tile: Isolation of cDNA encoding transcription factor Spl and functional analysis of A, Reference number: A29635; MUID:88080466; PMID:3319186
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A; Residues: 1-696 cKAD.
A; Cross-references: GB:J03133; NID:g339517; PIDN:AAA61154.1; PID:g339518
R; Ragoussis, J.; Senger, G.; Mockridge, I.; Sanseau, P.; Ruddy, S.; Dudley, K.; Sheer, D
R; Ragoussis, J.; Sanger, G.; Mockridge, I.; Sanseau, P.; Ruddy, S.; Dudley, K.; Sheer, D
R; Ragoussis, J.; Sanger, G.; Mockridge, G.; Sanseau, P.; Ruddy, S.; Dudley, K.; Sheer, D
A; Title: A testis-expressed Zn finger gene (ZNF76) in human 6p21.3 centromeric to the MH
A; Reference number: A44256; MUID:93052398; PMID:1427894
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A; Astaus: preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid
A; Residues: 569-598 < RAG>
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A,Cross-references: GDB:127453; OMIM:189906
A,Map position: 19913.1-19q13.3
C,Keywords: DNA binding; transcription regulation; zinc finger
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A;Note: sequence extracted from NCBI backbone (NCBIP:125980)
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60000

279/3; 313/2; 349/3; 409/1; 485/3; 54

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-430,452-1872,'AC',1875 <RE3>
A;Residues: 1-630,452-1872,'AC',1875 <RE3>
Cxcoss-references: GB:M35105; NID:g203597; PIDN:AAA40967.1; PID:g203598
C;Superfamily: kinase-related protein ros; LDL receptor YWTD-containing repeat homology, C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; kinase-related if c protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mol. Cell. Biol. 6, 3000-3004, 1986
A,Title: Human c-ros-1 gene homologous to the v-ros sequence of UR2 sarcoma virus encode
A,Reference number: A25223; MUID:87064611; PMID:3023956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: tumor cells
A;Note: the mcf3 oncogene was formed by DNA rearrangement involving fusion of at least t
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A,Note: the differences after residue 2245 result from the authors' misinterpretation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NiAlternate names: protein-tyrosine kinase mcf3 (activated ros-1)
NiContains: protein-tyrosine kinase (EC 2.7.1.112) ros-1
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence revision 07-Oct-1994 #text_change 11-Jun-1999
C;Accession: A35512; A25223; A24421; A33081
R;Birchmeier, C.; O'Neill: K.; Riggs, M.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 4799-4803, 1990
A;Title: Characterization of ROS1 cDNA from a human glioblastoma cell line.
                                                                                                                                                                                                                                                                         A;Residues: 1-430,452-2338 <RE2>
A;Cross-references: GB:M35104; NID:g203595; PIDN:AAA40966.1; PID:g203596
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A;Residues: 1854-2261,'A',2263-2347 <BI2>
A;Cross-references: GB:M13880; NID:g337482; PIDN:AAA36580.1; PID:g337483
                                                                                                                                  A;Cross-references: GB:M35106; NID:g203599; PIDN:AAA40968.1; PID:g203600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;753-793/Domain: LDL receptor YWTD-containing repeat homology <YW3>F;1935-2214/Domain: protein kinase homology <KIN>F;1943-1951/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Birchmeier, C.; Birnbaum, D.; Waitches, G.; Fasano, O.; Wigler, M. Mol. cell. Biol. 6, 3109-3116, 1986
A.Title: Characterization of an activated human ros gene.
A;Reference number: A24421; MUID:87064625; PMID:3785223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A35512; MUID:90280463; PMID:2352949
A;Accession: A35512
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                                                                                                                                                                                                    from GB/EMBL/DDBJ
                             ;Status: preliminary; translated from GB/EMBL/DDBJ
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Indels:
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A;Residues: 1790-2245,'KFDSSEFSSFRCTVN' <MA2>
A;Cross-references: GB:M13368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
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Mol. Cell. Biol. 6, 3000-3004, 1986
                                                                                                                                                            A,Accession: 156752
A,Status: preliminary; translated
A,Molecule type: mRNA
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0.80%
                                                             A; Molecule type: mRNA
A; Residues: 1-2338 <RES>
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A:Accession: I73957
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                                                                                                                                                                                                                             phospholipase C beta 3 - human
NyAlternate names: phospholipase c beta-3, phosphoinositide-specific
C;Species: Howo sapiens (man)
C;Decises: Howo sapiens (man)
C;Date: 15-Vul-1995 #sequence revision 21-Vul-1995 #text_change 17-Mar-1999
C;Accession: S52099; A56833; A56834
S;Lagercrantz, J.; Carson, E.; Phelan, C.; Grimmond, S.; Rosen, A.; Dare, E.; Nordenskjd
Submitted to the EMBL Data Library, September 1994
A;Description: Genomic organization and complete cDNA sequence of the human phosphoinosi
A;Reference number: S52099
A;Accession: S52099
A;Accession: S52099
A;Accession: Draininary
A;Molecule type: DNA
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NyContains: protein-tyrosine kinase (EC 2.7.1.112) ros-1
Syspecies: Rattus norvegicus (Norway rat)
C;Bete: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 02-Jun-2000
C;Accession: 173957; 156752; 173956
Natushine, H.; Shibuya, M.
J. Virol. 64, 2117-2125, 1395
A;Title: Tissue-specific expression of rat c-ros-1 gene and partial structural similarit
A;Reference number: 156752; MJID:90219211; PMID:2139140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-1234 <LAG>
A;Residues: 1-1234 <LAG>
A;Cross-references: EMBL:237573

R;Across-references: EmBL:237573

R;Across-references: E.; Phelan, C.; Grimmond, S.; Rosen, A.; Dare, E.; Nordenskjc Genomics 26, 467-472, 1995

Genomics 26, 467-472, 1995

A;Title: Genomic organization and complete cDNA sequence of the human phosphoinositide-s A;Reference number: A56833; MUID:95331781; PMID:7607669

A;Accession: A56833
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A;Introns: 33/3; 59/3; 82/3; 129/3; 156/2; 174/2; 199/3; 233/2; 288/3; 338/1; 418/2; 446
A;Introns: 33/3; 1167/3
C;Superfamily: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase I; 1-phosphatid
Gdiefterase domain Y homology
F;319-468/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
F;589-709/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain Y hom
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Genomics 25, 568-569, 1995
A.Tille: Localization of the human phosphatidylinositol-specific phospholipase C beta-3
A.Reference number: A56854; MUID:95309927; PMID:7789993
A.Rocession: A56854
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                                                                        217 AGTICTGGTCGGGGTAGTCCACGAAGG 191
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                                GATGCCCGCTTAGCTTCTCCATGGCTA
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A;Residues: 1-200 <LA2>
A;Cross-references: GB:Z37544
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A; Residues: 1-193 <SIN>
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: F72580
E;Accession: F72580
E;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; AyTtle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy A;Accession: F72580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <KAW>
A;Cross-references: DDBJ:AP000062; NID:g5105244; PIDN:BAA80931.1; PID:d1044717; PID:g51
C;Genetics:
                                                                                                 hypothetical protein APE1925 - Aeropyrum pernix (strain K1)
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C;Species: mitochondrion Limulus polyphemus (Atlantic horseshoe crab)
C;Accession: T12121
R;Staton, J.L.; Daehler, L.L.; Brown, W.M.
Mol. Biol. Evol. 14, 867-874, 1997
A;Title: Mitochondrial gene arrangement of the horseshoe crab Limulus polyphemus L.: Con A;Reference number: Z17427; MUID:97398711; PMID:9254925
A;Accession: T12121
A;Accession: T12121
A;Accession: T12121
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A,Residues: 1-63 <STA>
A,Cross-references: EMBL:AF002647; NID:g2316048; PID:g2316055; PIDN:AAC47689.1
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Conservative: Mismatches: Indels:

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This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92365105; PubMed=1323689; de Wind N. Domen J., Berns A.; de Wind N. Domen J., Berns A.; herpeviruses encode an unusual protein-serine/threonine kinase which is nonessential for growth in cultured cells."; J. Virol. 66:5200-5209(1992).
-: FUNCTION: PROTEIN-SERINE/THREONINE KINASE NONESSENTIAL FOR GROWTH
                                           Q9zjc5
P39370
Q9blx4
003478
P46636
P28334
P28564
P56496
P56496
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P60020
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Q01042
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Q9h6i2
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P10619
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Q64733
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InterPro; IPR00719; Prot kinase.

InterPro; IPR008719; Ser Thr pkin AS.

PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS0011; PROTEIN KINASE DOM; 1.

PROSITE; PS0011; PROTEIN KINASE DOM; 1.

PROSITE; PS0011; PROTEIN KINASE DOM; 1.

PROSIPCE; PS0011; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
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SX17 MOUSE
FXB2 MOUSE
HEMY HAEIN
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UMP1_ARATH
IE68_HSVSA
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NCBI_TaxID=10349;
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Q53719
                                                                                             July 16, 2004, 10:45:36 ; Search time 32 Seconds
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                  using frame plus n2p model
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FIBB HUMAN
SP1 MOUSE
SP1 HUMAN
SP1 RAT
KROS HUMAN
FTSB RALSO
N551_SOYBN
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Y915 MYCBO
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SEQUENCE FROM N.A.
MEDLINE=83283433; PubMed=6688356;
MEDLINE=83283433; PubMed=6688356;
Chung D.W., Que B.W.;
"Characterization of complementary deoxyribonucleic acid and genomic deoxyribonucleic acid for the beta chain of human fibrinogen.";
Biochemistry 22:3244-3250 (1983).
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Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
"Human fibrinogen: sequence, sulfur bridges, glycosylation and some
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (In) Liu C.Y., Chien S. (eds.); Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
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                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

BEDLINE-91344740; PubMed=2102623;
Chung D.W., Harris J.E., Davie E.W.;
"Nucleotide sequences of the three genes coding for human
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                                       D5C69AD75E42309B CRC64;
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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Mismatches:
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MEDLINE=79124640; PubMed=420779;
Watt K.W.K., Takagi T., Doolittle R.F.;
                                                                                                                                                           2 GCAGCGGAGGAGGCGAGGAGCGCCGGG 28
                                                                                                                                                                                                                                                                                                                                                                              fibrinogen.";
Adv. Exp. Med. Biol. 281:39-48(1990).
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01-JUL-1993
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MEDINE=99175089; PubMed=10074346; Bverse S.J., Spraggon G., Veerapandian L., Doolittle R.F.; Conformational changes in fragments D and double-D from human fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide."; Biochemistry 38:2941-2946 (1999).
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two
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"Crystal structures of fragment D from human fibrinogen and its crosslinked counterpart from fibrin.";
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MEDILINE-992923359; PubMed=9628725;
Everse S. J. Spragon G., Veerapandian L., Riley M., Doolittle
"Crystal structure of fragment double-D from human fibrin with
                                                                                                      SEQUENCE OF 31-148, AND DISULFIDE BONDS.
MEDILHE-76225080; PubMed=936108;
Blombaeck B., Hessel B., Hosy D.;
"Disulfide bridges in NH2-terminal part of human fibrinogen.";
"Amino acid sequence of the beta chain of human fibrinogen."; slochemistry 18:68-76(1979).
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Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton "Studies on fibrinopeptides from primates.";
Acta Chem. Scand. 19:1788-1789(1965).
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                                                                                                                                                                                                                                                                                                                                                       MEDLINE=87146483; PubMed=3029722;
Huber P., Dalmon J., Courtois G., Laurent M., Assouline
Marguerie G.;
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MEDLINE=97472408; PubMed=9333233;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beta gene.";
Nucleic Acids Res. 15:1615-1625(1987)
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Henschen A., Lottspeich F., Kehl M.,
"Covalent structure of fibrinogen.";
Ann. N.Y. Acad. Sci. 408:28-43(1983).
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Doollttle R.F.;
Tebrinogen and fibrin.";
Annu. Rev. Biochem. 53:195-229(1984).
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MEDLINE=87146483; PubMed=3029722;
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Biochemistry 37:8637-8642(1998).
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MEDLINE=77245999; PubMed=891553;
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                                                                                                                                                                                                                                                 Thromb. Res. 8:639-658(1976)
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VARIANT NAPLES THR-98.
MEDLINE=92346664; PubMed=1634610;
KOOPMEN J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;
Molecular basis of fibrinogen Naples associated with defective thrombin binding and thrombophilia. Homozygous substitution of B beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Characterization of single-nucleotide polymorphisms in coding regions
 Tanaka A., Litvinovich S.V., Medved L.V., Haudenschild C.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99318093; PubMed=10391209; Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
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MEDLINE=85157605; PubMed=3156856;
Liu C.Y., Koehn J.A., Morgan F.J.;
"Characterization of fibrinogen New York 1. A dysfunctional fibrinogen with a deletion of B beta(9-72) corresponding exactly to exon 2 of the gene.";
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Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi
Asakura S., Shirakawa S.;
                                   The interaction of fibulin-1 with fibrinogen. A potential role
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MEDLINE=20129589; PubMed=10666208;
Duga S., Assella R., Santagostino E., Zeinali S., Simonic T.,
Malcovati M., Mannucci P.M., Tenchini M.L.;
"Missense mutations in the human beta fibrinogen gene cause
congenital afibrinogenemia by impairing fibrinogen secretion.";
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                                                                          Biol. Chem. 270:19458-19464(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 Ala-->Thr.";
J. Clin. Invest. 90:238-244(1992).
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                                                      hemostasis and thrombosis.";
                                                                                                               VARIANT BALTIMORE-2 LYS-478
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Tran H.,
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[26] VARIANT CONGENITAL AFIBRINOGENEMIA CYS-196.

MEDLINE=21361164; PubMed=11468164;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2).

MEDLINE=96016118; PubMed=7568082;
Persengiev S.P., Saffer J.D., Kilpatrick D.L.;
"An alternatively spiled form of the transcription factor Spl
containing only a single glutamine-rich transactivation domain.";
Proc. Natl. Acad. Sci. U.S.A. 92:9107-9111(1995).
Lounes K.C., Lefkowitz J.B., Henschen-Edman A.H., Coates A.I., Hantgan R.R., Lord S.T.; "The impaired polymerization of fibrinogen Longmont
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Yajima S., Lee S.H., Minowa T., Mouradian M.M.;
"Sp family transcription factors regulate expression of rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 3 C2H2-type zinc fingers
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Mismatches:
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Matches:
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-!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS:
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DNA Cell Biol. 17:471-479(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
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analysis of the DNA binding domain.";
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                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  and for commercial
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                                                                                    EMBL; AF002.00, ABB35321.1; -
EMBL; X60136; CAA42721.1; -
EMBL; X60136; CAA42721.1; -
HSSP; P08047; LSP1.
MGD; MGI:98372; SP1.
GO; GO:00053700; F:transcription factor activity; IMP.
GO; GO:000535; P:regulation of transcription, DNA-dependent; IMP.
InterPro; IPR007097; Zf C2H2.
Pfam; PF00096; Zf C2H2; 3.
ProDom; PD000003; Znf C2H2; 3.
SMARI; SM00355; ZnF C2H2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takahara T., Kanazu S., Yanagisawa S., Akanuma H.;
Heteroganeous Spl mRNAs in human HepG2 cells include a product of
homotypic trans-splicing.";
J. Biol. Chem. 275:38067-38072 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                 SMART; SM00355; ZnF CZH7; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.
Transcription regulation; Activator; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; Glycoprotein; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haggart M.H., Ladurner A.G.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
  λq
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform 2).
/FTId=VSP 007376.
V -> G (IN REF. 2).
14CD12BBC58CF921 CRC64;
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  Usage
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Mismatches:
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  modified and this statement is not removed.
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Matches:
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C2H2-TYPE 2.
C2H2-TYPE 3.
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SEQUENCE OF 1-558 FROM N.A.
SEQUENCE OF 1-558 FROM N.A.
MEDLINE=20545561; PubMed=10973950;
                                                                          EMBL; AF062566; AAC16484.1; -.
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SEQUENCE OF 4-785 FROM N.A.
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Best Local Similarity:
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654
684
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MEDLINE-96224025; PubMed-8626793;

MEDLINE-96224025; PubMed-8626793;

The Parks C.L., Sheak T.,

"The serotonin la receptor gene contains a TATA-less promoter that responds to MAZ and Spl.";

J. Biol. Chem. 27114417-4430(1996).

ACTIVATES MRNA SYNTHEISI FROM GENES FLEMENTS AND SELECTIVELY ACTIVATES MRNA SYNTHEISI FROM GENES THAT CONTAIN FUNCTIONAL RECOGNITION SITES. CAN INTERACT WITH G/C-RICH MOTIFS FROM SEROTOMIN RECEPTOR PROMOTERS.

-1- SUBGELLUIAR LOCATION: Nuclear.

-1- SUBGELLUIAR LOCATION: Nuclear.

-1- PTM: O-Glycosylated; contains N-acetylglucosamine side chains.
                                                                                                                                                                                                                                                                                                                                 Handschug K., Huebner A.; "Sequencing of the 5' end of human transcription factor SP1 mRNA."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE=89003041; PubMed=3139301;
Jackson S.P., Tjian R.;
G-91ycosylation of eukaryotic transcription factors: implications for mechanisms of transcriptional regulation.";
Cell 55:125-133(1988).
                                                                         SEQUENCE OF 1-109 FROM N.A.
Nicolas M., Noe V., Ciudad C.J.;
Nicolas M., Noe V., Ciudad C.J.;
Supression of transcription factor Spi mRNA in mammalian cells.";
Submitted (APR-2000) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR OF 654-684 AND 684-712.
MEDLINE=97218212; PubMed=9065444;
Narayan V.A., Kriwacki R.W., Caradonna J.P.;
"Structures of zinc finger domains from transcription factor Spl.
Insights into sequence-specific protein-DNA recognition.";
J. Biol. Chem. 272:7801-7809(1997).
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EMBL, AB039286; BAB13476.1; --
EMBL, J03133; AAAG1154.1; --
EMBL, AF255682; AAF78781.1; --
EMBL, AJ272134; CAB75345.1; --
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                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-98 FROM N.A.
Cell 51:1079-1090(1987).
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MIM; 189906; -.
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PDB; 1SP1; 21-APR-97.
PDB; 1SP2; 21-APR-97.
TRANSFAC; T00759; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transcription element of the rat P-4501A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: O-glycosylated; contains N-acetylglucosamine side chains (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
SIMILARITY: BELONGS TO THE SP1 FAMILY OF C2H2-TYPE ZINC-FINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Imataka H., Sogawa K., Yasumoto K., Kikuchi Y., Sasano K., Kobayashi A., Hayami M., Fujii-Kuriyama Y.;
"Two regulatory proteins that bind to the basic transcription ele (BTE), a GC box sequence in the promoter region of the rat P-4501 gene ";
EMBO J. 11:3663-3671(1992).

-i- FUNCTION: BINDS TO GC BOX PROMOTERS ELEMENTS AND SELECTIVELY ACTIVATES MRNA SYNTHESIS FROM GENES THAT CONTAIN FUNCTIONAL
              r protein; Repeat; Glycoprotein; 3D-structure 650
Transcription regulation; Activator; Zinc-finger; Metal-binding;
                                                                 SEQUENCE).
                                                                                                                                                         43893DBF6518B9EA CRC64;
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                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                              D -> G (IN REF. 3;
S -> F (IN REF. 3;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            788 AA
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                        C2H2-TYPE 1.
C2H2-TYPE 2.
C2H2-TYPE 3.
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                                                                                                                                                                                                                                                                                                               893 ATCTCTTCGGCTAGTTTGGTCTCATCT 867
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SUBCELLULAR LOCATION: Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93010958; PubMed=1356762;
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01-APR-1993 (Rel. 25, Last seq
10-OCT-2003 (Rel. 42, Last ann
                                                                                                                                                        80693 MW;
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366
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657
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666
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              Nuclear
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HSSP; P08047; 1SP1.
TRANSFAC; T00754; -.
                                                                                                                                                        785 AA;
                                                                                                                                                                                                                                    Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                         626
656
686
686
670
657
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666
670
678
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          DNA-binding; N
ZN FING 62
ZN FING 65
ZN FING 66
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CONFLICT
STRAND
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SP1_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90280463; PubMed=2352949;
Birchmeier C., O'Neill K., Riggs M., Wigler M.;
Characterization of RoS1 cDNA from a human glioblastoma cell line.";
Proc. Natl. Acad. Sci. U.S.A. 87:4799-4803(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
receptor subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P08922; Q15368;
01-NOV-1998 (Rel. 09, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Proto-oncogene tyrosine-protein kinase ROS precursor (EC 2.7.1.112)
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MEDLINE=87064625; PubMed=3785223;
Birchmeier C., Birnbaum D., Waitches G., Fasano O., Wigler M.;
Characterization of an activated human ros gene.";
Mol. Cell. Biol. 6:3109-3116(1986)
-!- FUNCTION: THIS IS A PROBABLY A CELL GROWTH OR DIFFERENTIATION
FACTOR RECEPTOR WITH A TYROSINE-PROTEIN KINASE ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
InterPro; IPR007087; Znf_C2H2.

Pfam; PF00096; zf-C2H2; 3.

ProDom; PD000003; Znf_C2H2; 2.

SMART; SM00355; Znf_C2H2; 3.

PROSITE; PS00028; ZiNC_FINGER_C2H2_1; 3.

PROSITE; PS00157; ZINC_FINGER_C2H2_2; 3.

Transcription regulation; Activator; Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat; Glycoprotein.

ZN_FING 629 683 C2H2_TYPE 1.

ZN_FING 659 683 C2H2_TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsushime H., Wang L.-H., Shibuya M.;
Human C.-ros-1 gene homologous to the v-ros sequence of UR.
virus encodes for a transmembrane receptorlike molecule.";
Mol. Cell. Biol. 6:3000-3004(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mismatches:
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Matches:
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MEDLINE=87064611, PubMed=3023956;
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                                                                                                                                                                                                              788 AA;
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Best Local Similarity:
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Pred. No.:
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N-LINKED (GLCNAC. ..) (POTENTIAL).
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-:- SUBGNIT: May interact with ftsL (By similarity).
-:- SUBCELPULAR LOCATION: Type II membrane protein. Inner membrane (By cential). Colocalizes with ftsL to the division site (By similarity).
-:- SIMILARITY: Belongs to the ftsB family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salamoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Fenard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., "Gelseme sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                                                                  E14F3DFD410C1D2A CRC64;
                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                      Mismatches:
Indels:
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28-FEB-2003 (Rel. 41, Last annotation update)
Cell division protein fitsB homolog.
FTSB OR RSC1130 OR RSO4623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AA
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MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                  AA; 263956 MW;
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InterPro; IPR007060; DivIC.
Pfam; PF04977; DivIC; 1.
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Q8Y0<u>B</u>4;
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R MIM; 155022; -.

R GO:0005890; C:membrane fraction; TAS.

R GO:0005890; C:sodium/potassium-exchanging ArPase complex; TAS.

R GO:0004713; F:protein-tyrosine kinase activity; TAS.

R GO:0004712; F:receptor activity; TAS.

R GO:0007165; P:signal transduction; TAS.

R InterPro; IPR003957; FN III-like.

R InterPro; IPR003957; FN III-like.

R InterPro; IPR00119; Prot kinase.

InterPro; IPR001245; Tyr pkinase.

R InterPro; IPR001245; Tyr pkinase.

R Pfam; PF00041; fn3; 7.

R Pfam; PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R PRINTS; PRO0109; TYRENCY, 1.

R SMART; SM00001; Prot_kinase; 1.

R SMART; SM00109; TYRC; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE TYR; 1.

R PROSITE; PS00119; PROTEIN KINASE DM; 1.

R PROSITE; PS00119; PROTEIN KINASE DM; 1.

R PROSITE; PS0011; PROTEIN KINASE DM; 1.

R PROSITE; PS0011; PROTEIN KINASE DM; 1.

Transferase; Tyrosine-profein kinase; Receptor; Transmembrane; Signal.

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CYTOPLASMIC (POTENTIAL).
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   entities requires a license agreement (or send an email to license@isb-sib.ch)
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EMBL; M3599; AAA60277.1; --
EMBL; M3599; AAA60277.1; --
EMBL; M3591; AAA60277.1; JOINED.
EMBL; M13592; AAA60277.1; JOINED.
EMBL; M13593; AAA60277.1; JOINED.
EMBL; M13594; AAA60277.1; JOINED.
EMBL; M13595; AAA60277.1; JOINED.
EMBL; M13595; AAA60277.1; JOINED.
EMBL; M13596; AAA60277.1; JOINED.
EMBL; M13598; AAA60277.1; JOINED.
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EMBL; M13598; AAA60277.1; JOINED.
EMBL; M13598; AAA60277.1; JOINED.
EMBL; M13698; AAA36580.1; ALT_TERM.
HSSP; PO8631; JAD5.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-cv. Williams; TISSUE-Root;
MEDLINE=940303074; PubMed=8400132;
MEDLINE=940303074; PubMed=8400132;
MEDLINE=940303074; PubMed=8400132;
"Characterization of the soybean early nodulin cDNA clone GmENOD55.";
Plant Mol. Biol. 22:1167-1171(1993).
-! SUBCELLUIAR LOCATION: Peribacteroid membrane (Potential).
-! DEVELOPMENTAL STAGE: Expressed at early stages of nodule development, Maximal expression is seen in nodules from 14-day-old plants after which levels decrease.
-! INDUCTION: During nodulation in legume roots after Rhizobium infection, and after release of bacteria from the infection
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viriâiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae, Glycine.
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InterPro; IRR088972; Cupredoxin.
InterPro; IRR083245; Ployanin like.
Pfam; PF02288; Cu bind like; I
ProDom; PD003122; Ployanin like; 1.
Nodulation; Glycoprotein; Nitrogen fixation; Signal; Membrane.
Cell division; Transmembrane; Inner membrane; Coiled coil;
                                POTENTIAL.
PERIPLASMIC (POTENTIAL).
COILED COIL (POTENTIAL).
E4A926F7359C6C9C CRC64;
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                      CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Early nodulin 55-1 precursor (N-55-1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EARLY NODULIN 55-1.
PLASTOCYANIN-LIKE.
                                                                                                                                Conservative:
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Indels:
                                                                                                                                                                                                                                                                                     137 AA.
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                      3 CY
21 PC
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12658 MW;
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           Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain cortex;

Wurch T., Lestienne F., Colpaert F.C., Pauwels P.J.;

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: This is one of the several different receptors for 5-hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cyclase activity (By similarity).
-!- SUBCELLUIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other SHT-1 subtype receptors.
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Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y11867; CAA72615.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm i. 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSTTE; PS00237; G PROTEIN RECEP_F1_1; FALSE_NEG.
PROSTTE; PS02237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family.
NON TER 1 class CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL).
  N-LINKED (GLCNAC. . .) (PO 988DE6F89A2E0BE0 CRC64;
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CYTOPLASMIC (POTENTIAL)
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                   US-09-270-437D-6 (1-3412) x N551_SOYBN (1-137)
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  68 N-
14857 MW;
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15-JUL-1998 (Rel. 36, Last seq
10-OCT-2003 (Rel. 42, Last ann
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107
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116
141
>150
  68
137 AA;
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                                                                                                                                              Percent Similarity:
                                                                         Alignment Scores:
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P79399;
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TRANSMEM
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Indels:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydroxytryptamine (serotonin), a biogenic hormone that functions as a neurotransmitter, a hormone, and a mitogen. The activity of this receptor is mediated by G proteins that inhibit adenylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sgard F., Faure C., Graham D., "Evidence for 5-HTID alpha receptor subtype expression in canine large coronary arteries and saphenous vein."; Cardiovasc. Res. 31:793-799(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cyclase activity.
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
Strongest to the other 5HT-1 subtype receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.JUL-1998 (Rel. 36, Last sequence update)
10.CCT-2003 (Rel. 42, Last annoctation update)
5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor) (5-HT1B) (5-HT1D subtype beta) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO237; G PROTEIN RECEP F1 1; PARTIAL.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Lipoprotein; Palmitate.
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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      Conservative:
Mismatches:
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STRAIN=Beagle, and Alsatian; TISSUE=Artery;
MEDLINE=96296365; PubMed=8763409;
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InterPro; PR000276; GFCR_Rhodpsn.
Pfam; PP00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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15-JUL-1998 (Rel. 36, Last seq
10-OCT-2003 (Rel. 42, Last ann
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Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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P79250;
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                                                            Query Match:
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                                                                                                                                                                                                                                                                                                                       RESULT 10
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Conservative: Mismatches:

100.00%

Percent Similarity: Best Local Similarity:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MUSO, ATCC 700699, and N315;
STRAIN=MUSO, ATCC 700699, and N315;
STRAIN=MUSO, ATCC 700699, and N315;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Katto C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-2240717; PubMed=12044378; Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.; "Genome and virulence determinants of high virulence community-acquired MRSA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=NCTC 8325;
BDDLINE=P4131293;
BOTCHARCH S.A., Babwah A.V., Jayaswal R.K.;
Sequence analysis of the region downstream from a peptidoglycan "Sequence encoding gene from Staphylococcus aureus NCTC8325.";
Gene 137:253-258(1993)
-i- SIMILARITY: BELONGS TO THE THIJ / PPPI FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical protein SAV1875/SAL692/MW1815 (ORFI).
SAV1875 OR SAL692 OR MW1815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus aureus (strain Mu50 / ATCC 700699), Staphylococcus aureus (strain N315), Staphylococcus aureus (strain MW2), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 196620, 1280;
                                                                                                                                                                                                                                                                                                                                                                                         171 AA
                                                                                                   US-09-270-437D-6 (1-3412) x 5H1B CANFA (1-161)
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EMBL; AP004828; BAB95680.1; -.
EMBL; L19300; AAA18514.1; -.
EMB, E89975; B89975.
MEROPS; C56.UPW; -.
InterPro; IPR006286; Peptidase_C56.
                                                                                                                                                                          2547 TCTGGATCACCTGTGTATGTCAAC
                                                                                                                                                                                                                                            SerGlySerProvalTyrValAsn
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                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus.
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ID YI75 STA
AC Q53719;
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Caenorhabditis elegans.
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DOMAIN 2 74
DOMAIN 84 205
VARSPLIC 1 128
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                                                                                                                                                                                        SEQUENCE FROM N.A.
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                RESULT 13
YSX2_CAEEL
                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein gene, crps-7.";
Curr. Genet. 31:139-143(1997).
-!- SIMILARITY: Belongs to the S7E family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lerula P.J.;
"Cloning and characterization of a Neurospora crassa ribosomal
                                                   A571A08B0FD0D719 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 AA; 22819 MW; 94D87756FFE37798 CRC64;
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Mismatches:
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                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
RPS-7 OR CRPS-7.
                                                                                                                                                                                                                                                                            202 AA
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InterPro; IPR002818; ThiJ/PfpI.
Pfam; PF01965; DJ-1 PfpI; 1.
IGRFAMs; TIGR01382; PfpI; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 171 AA; 18632 MW; A571A08B0
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PIR, T46586; T46586.
InterPro, IPR000554; Ribosomal S7E.
Pfam, PF01251; Ribosomal S7e.
Prodom; PD006276; Ribosomal S7e.
Prodom; P200948; Ribosomal S7E, 1.
                                                                                                                                                                                                                2527 GGAAGGACACTCACGGCAGTTCTG
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MEDLINE=97174111; PubMed=9021131;
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043105;
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Query Match:
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/FTId=VSP 005906.
/FTId=VSP 005906.
/FTId=VSP 005907.
LKREASRSRSPLPAKDRSRT -> FHSSMRNQYHLQAHIAM
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SRSSP - MEKTHANTMEKDWRABLCALEWRWIAERHAA
MTWMRRDHHDDVPALLDVUHVLHQEDVPALVIAADDVP
BAPPDDDHQFVKVVAEANPVRRARKETLMVNYQVISIHFSF
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FEDSRDAEDACHDLDGKTMEGSSMRLVVEMARGKPRGNDRH
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Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=4; Comment=Experimental confirmation may be lacking for some
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SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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REMBL, U28738; AAK68399.2; -.

REMBL, U28738; AAK72066.2; -.

REMBL, U28738; AAK72066.2; -.

ROTHORPO, T28D9.2a; CE29826.

ROTHORPO, T28D9.2b; CE29826.

ROTHORPO, T28D9.2d; CE29828.

ROTHORPO, T28D9.2d; CE29828.

ROTHORPO, T28D9.2d; CE28094.

ROTHORPO, T28D9.2d; CE28094.

ROTHORPO, T28D9.2d; CE28094.

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ROTHORPO, T28D9.2d; CE2982.

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ROTHORPO, T28D9.2d; CE2982.

ROTHORPO, T28D9.2d; CE2982.

ROTHO
YSX2_CAEEL STANDARD; PRT; 208 AA. Q10021; Q95ZNO; Q95ZNZ; Q10021; Q95ZNO; Q95ZNZ; Q10-OCT-1996 (Rel. 34, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 49-FEB-2003 (Rel. 41, Last annotation update) Hypothetical RNA-binding protein T28D9.2 in chromosome II. T28D9.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston R.;
submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fulton L.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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Isold=Q10021-2; Sequence=VSP_005908, VSP_005910;
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Isoid=Q10021-3; Sequence=VSP_005906, VSP_005907;
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STRAIN-GOOL | GOI | ATCC BAA-199 | DSM 3647 | OCM 88;

MEDLINE=22120827; PubMed=12125834;

MEDLINE=22120827; PubMed=12125834;

MARTINEZ-Arias R., Johanna A., Hartsch T., Merkl R., Schmitz R.A.,

Martinez-Arias R., Henne A., Wiezer A., Bacumer S., Jacobi C.,

Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,

Brueggemann H., Lienard T., Christmann A., Boemecke M., Steckel S.,

Fritz H.-J., Gottschalk G.,

"The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea."

J. Mol. Microbiol. Biotechnol. 4:453-461(2002).

--- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
                                              SRDGSNRSVSRSPSPGSPKD -> QLRANISVSYSSPLDSD
SKCKNYILGSVKRRNLVHHCQOKIRAEPEVDLPQRTAEIE
SAA (in isoform d).
/FTId=VSP_005909.
                     KREASRSRSPLPAKDRSRTRSGSPPKNGGDRKRSVSRGRSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanosarcina mazei (Methanosarcina frisia).
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP, MF 00291, -; 1.
InterPro; IPR001865; Ribosomal S2.
InterPro; IPR001865; Ribosomal S2.
InterPro; IPR0013070; Ribosomal S2.
Pfan, PR001318; Ribosomal S2; 1.
PRINTS; PR00395; RIBOSOMĀLS2.
TIGRFAMS; TIGR01012; Sa S2 B A; 1.
PROSITE; PS00962; RIBOSOMĀL S2 1; 1.
PROSITE; PS00963; RIBOSOMĀL S2 2; 1.
Ribosomal protein; Complete proteome.
SEQUENCE 224 AA; 24625 WW; 144D106450BA125E CRC64;
                                                                                                                                                                 'FTId=VSP_005910.
A33CAFC78D74A6F8 CRC64;
                                                                                                                                                                                                                                                           Missing (in isoform b).
                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
    005908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 AGTCCACGAAGGCGTAGCCGGACT 179
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                                                                                                                                                                                    208 AA; 23946 MW;
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8.00
100.00%
100.00%
0.73%
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                     208
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28-FEB-2003 (Rel. 41,
30S ribosomal protein
RPS2P OR MM1760.
                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2209;
                                                                                                                                        167
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                                                                                                                                                                                    SEQUENCE
                                                                                                                                        VARSPLIC
                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08PW41;
                                                                                                                                                                                                                                                                                                                                                     Query Match:
                                                                                                                                                                                                                                                        Pred. No.:
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ID RS2_M
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Length:

53.6

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REQUIRICE FROM N.A.

SEQUENCE FROM N.A.

REQUIRIN=21929760; PubMed=11932238,

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Allan N., Naylor J., Strange-Thomann N., DeArellano K., Johnson R.,

RA Linton L., McEwann P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McEwan P., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

RA Hedderich R., Ingram-Smirth C., Kuettner H.C., Krzycki J.A.,

RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Gerve J.N., Smith K.,

RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

RA Fritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;

RA Metcalf W.W., Birren B.;

RA Metcalf W.W., Birren B.;

RA Metcalf W.W., Subersita acetivorans reveals extensive metabolic

RI "The genome of Methanosarcina acetivorans reveals extensive metabolic

RI Genome Res. 12:532-542(2002).

C. -- SIMIARITY: Belongs to the S2P family of ribosomal proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibs-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina
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Conservative:
Mismatches:
Indels:
Matches:
Conservative:
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28-FEB-2003 (Rel. 41, Last seguence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         225 AA
                                                                                    Indels:
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                                                                                                                                                                  US-09-270-437D-6 (1-3412) x RS2_METMA (1-224)
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                                                                                                                                                                                                                                                                          90
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PROSITE; PS00962; RIBOSOMAL 52 1; 1.
PROSITE; PS00963; RIBOSOMAL S2 2; 1.
                                                                                                                                                                                                                                                         83 ArgValAlaSerLysLeuLeuSer
                                                                                                                                                                                                                         2496 CGGGTGGCCTCAAAGCTCCTCT
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SEQUENCE 225 AA; 24779 MW;
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100.00%
0.73%
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8.00
100.00%
100.00%
0.73%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methanosarcina acetivorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30S ribosomal protein S2P. RPS2P OR MA0600.
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                         RS2 METAC
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                                                                                                                                                                                                                                                                                                                                    RESULT 15
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US-09-270-437D-6 (1-3412) x RS2\_METAC (1-225)

Qy Dp

Search completed: July 16, 2004, 11:18:44 Job time : 50 secs

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APPRODECE FROM N.A.

RA SIGNEME PROM N.A.

RA Zhang J.Y., Chan E.K., Peng X.X., Tan E.M.;

RA Zhang J.Y., Chan E.K., Peng X.X., Tan E.M.;

RT "A novel cytoplasmic protein with RNA-binding motifs is an autoantigen RT "A novel cytoplasmic protein with RNA-binding motifs is an autoantigen RT "A novel cytoplasmic protein with RNA-binding motifs is an autoantigen RT "A novel cytoplasmic Protein With RNA-binding motifs is an autoantigen RT "A novel cytoplasmic Protein With RNA-binding RC --- SIMILARITY: CONTAINS 4 KH DOMAINS.

DR EMBL, AF057352; AAD31596.1; ---

DR GO: GO:0005737; C:cytoplasmi TAS.

DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.

DR GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
                                                                                                                                                                       Q862j9 mus musculu Q9cpn8 mus musculu Q7tp50 rattus norv Q86xb1 homo sapien Q014h1 chamydophi Q9uiw homo sapien Q9tv01 deinococcus Qariy1 neurospora Q25x1 listeria mo Q25x1 listeria mo Q3cac mus musculu Q82se0 nitrosomona Q81se0 nitrosomona Q8fg6 corynabacte Q18705 caenorhabdi Q8fg6 corynabacte Q18705 caenorhabdi Q8f410 rattus norv Q9cay1 arabidopsis Q9ti3 drosophila Q8tvv7 methanopyru Q8tvv7 mus musculu Q8vv7 mus musculu Q8vv1 mus musculu Q8vv1 mus musculu Q8vv1 mus musculu
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Q63131 rattus norv
Q63130 rattus norv
Q63132 rattus norv
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Q8q072 methanosarc
Q8i429 plasmodium
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08efb9 shewanella
                                xenopus lae
                                                                                           O8cgx0 rattus norv
O8brh1 mus musculu
                                                                                                                           Q80us9 mus musculu
O88477 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7xs11 oryza sativ
                                                            O42254 gallus gall
                                                                                                                                                           000425 homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286gd6 procambarus
                                                                          homod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               073932
                                                                             29nzi8
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Last annotation update)
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                                                                                                                                                           000425
Q8C2J9
Q9CPN8
Q7TP50
Q86VB1
                                                                                                                                                                                                                                       Q824H3
Q9UIW1
Q9RV01
Q8NIY1
Q926X1
                                                                                                                                                                                                                                                                                                                      Q9DAE2
Q82SE0
Q8JGN3
Q8FLQ8
Q18705
Q8P646
Q94D52
Q8K4R0
                                                           042254
Q9NZI8
Q8CGX0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   080072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q7XS11
Q9LXTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q63130
Q63132
                                                                                                                           Q80US9
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Q8TVS7
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                                                                                                             Q8BRH1
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559
623
704
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1086
1135
1226
1854
2317
2338
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                                                                                                                                                                                                          NCBI_TaxID=9606;
 Q9Y6M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9Y6M1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
 29Y6M1
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-MODEL=frame+ n2p.model -DEV=Xlp
-D=/Cogn_21/USFPTO_Spool p/US09270437/runat_16072004_113127_13955/app_query.fasta_1.3591
-D=/Cogn_21/USFPTO_Spool p/US09270437/runat_16072004_113127_13955/app_query.fasta_1.3591
-D=CPFEREMBL_S=-CPFMT=fastan -SUFFTX=01490.rspt -MINMATCH=0.1 -LOOPECL=0
-LOOPEXT=0 -\text{To MITS}=bits -START=1 -END=-1 -MATRIX=01490 -TRANS=human40.cdi
-LIST=AD-LIGN=200 -TRR_SCORE=quality -TRR_MIN=1 -AD-LIGN=15 -MODE=LOCAL
-USFR=US09270437_@CGN_1_1_283_@runat_16072004_113127_13955 -NCPU=6 -ICPU=3
-NO_WMAD_LARREDUERY -NGG_SCORES=0 -MINIT=0FPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
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13249.823 Million cell updates/sec
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                                                                                                                                                                                                             Description
                                                                                                             July 16, 2004, 10:57:48 ; Search time 162.5 Seconds
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                             using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                       1017041 segs, 315518202 residues
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sp_unclassified:*
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sp_mammal:*
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sp_bacteriap:*
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sp_phage:*
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sp_bacteria:*
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sp_rodent:*
sp_virus:*
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Maximum DB seq length: 2000000000
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1120
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Match Length DB
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Ygapop 60.0 , Y
Fgapop 6.0 , E
Delop 6.0 , I
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                                                                               protein search,
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                                                                                                                                                                                              score:
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                                                                                                                                                                                                               Sequence:
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280 696 300

1089 320

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CS7BL/6; TISSUE=Brain;

RA
STRAIN=238827; PublMed=12477932;

RA
STRAIN=288287; PublMed=12477932;

RA
Alternis R.L., Fetingold E.A., Grouse L.H., Derge J.G.,

RA
Alternis R.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA
Alternis R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA
Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.U.,

RA
BOSAS R.A., McEwan P.J., McKernan K.J., Malk J.A., Gunarathe P.H.,

RA
Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA
Villalon M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA
Rodiguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA
Jones S.J., Marra M.A.;

RA
Generation and initial analysis of more than 15,000 full-length human
                                                                                      281 AlakisasnGlyLeuValGlyAxgLeuIleGlyLysGluGlyAxgAsnLeuLysLysIle
                                                                                                                                         ATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTG
                                  261 IleMetGlnLysGluAlaAspGluThrLysLeuAlaGluGluIleProLeuLysIleLeu
                                                                                                                        GAACATGAAACAGGGACCAAGATAACAATCTCCATCTTTGCAGGATTTGAGCATATACAAC
                                                                      GGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAATT
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
10-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CS7BL/6; TISSUE=Brain;
Strausberg R.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BRO54552; AAH54552.1; -.
Hypothetical protein.
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           InterPro; IPPR004087; KH_dom.
InterPro; IPR004088; KH_type 1.
InterPro; IPR000504; RNA_rec_moc.
Pfam; PF00013; KH; 4.
Ffam; PF00076; rrm; 2.
SNART; SM00322; KH; 4.
SNART; SM00360; RRM; 2.
                                                                                                      PROSITE; PS50084; KH TYPE 1; 4.
PROSITE; PS50102; RRM; 2.
SEQUENCE 556 AA; 61842 MW; 1
GO:0009386; P:translational
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EMBL; AF161270; AAD45610.1; -.
EMBL; BC045873; AAH45873.1; -.
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Pfam; PF00076; rrm; 2.
SMART; SM00322; KH; 4.
PROSITE; PS50084; KH; TYPE_1; 4.
PROSITE; PS50102; RRM; 2.
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MEDLINE-2238257, PubMed=12477932;

MEDLINE-2238257, PubMed=12477932;

MEDLINE-2238257, PubMed=12477932;

MEDLINE-2238257, PubMed=12477932;

MALSCOUL S. P., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hisleh F.,

M. Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

M. Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

Rabey J., Helton B., Ketteman M., Madan A.M., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Generation and initial analysis of more than 15,000 full-length human
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 15, Last annotation update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Vgl RNA binding protein (Decapentaplegic and Vg-related 1, RNA binding
                                                                                                                                                                                                  219 ValAspIleHisArgLysGluAsnSerGlyAlaAlaGluLysProValThrIleHisAla
                                                                                                                                                                      GCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACTAAGCAGACCCAGTCCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Zhang Q., Yaniv K., Oberman F., Wolke U., Git A., Fromer M., Zhang Q., Yaniv K., Copernan F., Wolke B., Yisraeli J.K.; Taylor W., Meyer D., Standart N., Raz E., Yisraeli J.K.; "V91 RBP intracellular distribution and evolutionarily conserved expression suggest multiple roles during development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         582 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 AspGluThrLysLeuAlaGluGlu 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                             868 GATGAGACCAAACTAGCCGAAGAG 891
                           US-09-270-437D-6 (1-3412) x Q7TQF9 (1-545)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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STRAIN=AB; TISSUE=Body;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mech. Dev. 0:0-0(1999)
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DVR1RBP.
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1507 GGGCCACCGGAAGCCCAGTTCAAGGCCCAGGACGGATCTTTGGGAAACTGAAAGAGAA 1566
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KH domain-containing transcription factor B3.

Butaryota, Metazoa, Chordan Clawed frog).

Bukaryota, Metazoa, Chordan Crania, Vertebrata; Euteleostomi;

Amphiblia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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MEDLINE=92249652; PubMed=1577195;
Pfaff S.L., Taylor W.L.;
"Characterization of a Xenopus cocyte factor that binds to a developmentally regulated cis-element in the TFIIIA gene.";
Dev. Biol. 151:306-316(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffin D., Taylor W.L.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Havin L. Yanix K.,

Havin L. Strat A.,

Pressman Schwartz S., Standart N.M., Yisraeli J.K.;

Genes Dev. 0:0-0(1998).

-!- SIMILARITY: CONTAINS 4 KH DOMAINS.

EMBL, AF046335, AAB97457.1; -.

EMBL, AF0464335, AAC18597.1; -.

GO; GO:0003676; F:nucleic acid binding; IEA.

InterPro; IPR004089; KH dom.

InterPro; IPR004089; KH dom.

InterPro; IPR004089; KH dom.

InterPro; IPR00564; RNA_rec_mot.

Pfam; PF00013; KH; 4.
                                                                                                                                                                                                                                                                                                                                      63351 MW; 9DAE63200681B306 CRC64;
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Last annotation update)
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Conservative:
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ZFIN; ZDB-GENE-000308-1; dvr1rbp.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004089; KH-dom.
InterPro; IPR004089; KH-type.1.
InterPro; IPR00504; RNA_rec_mot.
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US-09-270-437D-6 (1-3412) x 073932 (1-594)
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                                                                            1690 GCAGAAGTC 1698
                                                                                             532 AlaGluVal 534
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Best Local Similarity:
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                                                                                                                                                                                                    1630 GCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACTGCAGAACTTAACCAGT 1689
                                                                                                                                                                                                                 VGI RNA binding procein variant D.

Kenopus laevis (African clawed frog).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Kenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Described From w. A.

MEDLINE-9828351; PubMed=9560341;

Deshler J.O., Highett M.I., Abramson T., Schnapp B.J.;

T. A highly conserved RNA-binding protein for cytoplasmic mRNA localization in vertebrates.";

Curr. Biol. 8:489-496(1998).

C. -I. SIMILARITY: CONTAINS 4 KH DOWAINS.

EMBL; AF055923; AAC41285.1; -..

EMBL; AF054034; AAC1858.1; -..

EMBL; AF056034; AAC1858.1; -..

EMBL; AF056034; KH type.1.

InterPro; IPR004089; KH type.1.

R InterPro; IPR004089; KH type.1.

R Pros. IPR0013; KH; 4.

Pram; Pr00013; KH; 4.

Pram; PR00015; rrm; 2.

R MART; SM0332; KH; 4.

SMART; SM0332; RH; 2.

SMART; SM0332; RH; 2.

SMART; SM03049; RRM; 2.

PROS. ITE; PS50102; RRM; 2.

SEQUENCE 594 AA; 65643 MW; 54CEA7BFF0856DD6 CRC64;
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
PROSITE; PS50084; KH; TYPE_1; 4.
PROSITE; PS50003; RRM; 2P=1; FALSE NGG.
PROSITE; RS00030; RRM; RNP 1; FALSE NGG.
SEQUENCE 593 AA; 65385 MW; 5A5AB4B4A1D55DF7 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Havin L., Git A., Elisha Z., Oberman F., Yaniv K., Pressman Schwartz S., Standart N.M., Yisraeli J.K., Genes Deev. 0:0-0(1998).
                                                                                               Length:
Matches:
Conservative:
Mismatches:
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Mismatches:
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Best Local Similarity:
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SEQUENCE FROM N.A.
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Query Match:
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Percent Similarity:
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1689
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RN [1]
RN SEQUENCE FROM N.A.
RDLINE-97220007; PubMed=9121465;
RA ROSS A.F., Oleynikov Y.S., Kislauskis E.H., Taneja K.L., Singer R.H.;
RT "Characterization of a beta-actin mRNA zipcode-binding protein.";
RI "Characterization of a beta-actin mRNA zipcode-binding protein.";
RI "Characterization of a beta-actin mRNA zipcode-binding protein.";
RI "Characterization of a beta-actin mRNA zipcode-binding protein.";
RI "Characterization of a beta-actin mRNA zipcode-binding protein.";
ROC :- SIMILARITY: CONTAINS 4 KH DOMAINS.

DR RED,; AF026527; AAB82295.1; --
GO, GO:000376; F:runcled acid binding; IEA.

DR InterPro; IPR004089; KH type. 1.

DR InterPro; IPR004089; KH type. 1.

DR Ffam; PF00013; KH; 4.

DR Ffam; PF00013; KH; 4.

SMART; SM00322; KH; 4.

SMART; SM00322; KH; 4.

SMART; SM00320; RRM; 2.

DR PROSITE; PS50084; KH TYPE. 1; 4.

DR PROSITE; PS50030; RRM; 2.

DR PROSITE; PS50102; RRM; 2.

DR PROSITE; PS003030; RRM; 1.

SRQUENCE 576 AA; 63271 MW; 01AAF2D1D81C8811 CRC64;
                                                   531
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
mRNA-binding protein CRDBP.
Endow sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
111—TaxID=9606;
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119
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                            576 AA.
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499 AlaGlyArgVallleGlyLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuThr 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CS7BL/6J;
MEDLINE=222546683; PubMed=12466851;
The FANTOM CONSORtium.
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaGlyArgVallleGlyLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuThr
                                                                                                 1630 GCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACTGCAGAACTTAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus mūscūlus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Insulin-like growth factor 2.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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MGD; MGI:1890357; Igf2bpl.
GO; GO:0003676; F:nucleic acid binding; IEA.
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  Indels:
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                                                          US-09-270-437D-6 (1-3412) x Q8CGX0 (1-577)
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InterPro; IPR004088; KH type_1.
InterPro; IPR000504; RNA_rec_mot.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PP00013; KH; 4.
Pfam; PP00076; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SM00322; KH; 4.
PROSITE; PS50084; KH TYPE_1; 4.
PROSITE; PS50084; KH TYPE_1; 4.
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                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            577 AA;
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Best Local Similarity:
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  Query Match:
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STRAIN-Sprague-Dawley;
Bom T., Singer R.H., Bassell G.J.;
Bom T., Singer R.H., Bassell G.J.;
Bom T., Singer R.H., Bassell G.J.;
Bom T., Singer R.H., Bassell G.J.;
Wolecular interactions between rZBPI and b-actin zipcode required for transport of mRNA and stimulation of spine growth.";
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, FSF41940, AAOLES10.11;
GO, GO.303676; F.nucleic acid binding; IEA.
InterPro; IPR004088; KH dom.
InterPro; IPR004088; KH type 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
              Panoutsakopoulos G., Kyriazoglou I., Voutzoulias S., Tsiapalis C.M., Kittas C., Agnantis N., Pandis N.;
"Ectopic expression of a KH-domain containing protein, highly homologous to both human IMP-1 and mouse CRD-BP, in benign and malignant mesenchymal tumores.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: CONTAINS 4 KH DOMAINS.
---SIMILARITY: CONTAINS 4 KH DOMAINS.
HSSP; P11940; 1CVJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 ArgMetValllelleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArgIle
  Trangas T., Dimitriadis E., Samiotaki M.,
                                                                                                                                                                                                                                                                      Pfam; PF00013; KH; 4. — — — Pfam; PP00013; KH; 4. — — Pfam; PP00076; TTTM; 2. SMART; SM00322; KH; 4. SWART; SM00360; RRM; 2. PROSITE; PS50084; KH TYPE_1; 4. SRQUENCE 577 AA; 63456 MW; 0749A060F252D81D CRC64;
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577 AA; 63436 MW; 0647676128FBD1EE CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Conservative:
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Matches:
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InterPro; IPR004089; KH dom.
InterPro; IPR004089; KH type 1.
InterPro; IPR000504; RNA_rec_mot.
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Pfam; PF00076; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
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Ioannidis P.,
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Genes Dev. 6:642-654(1992).
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Pred. No.:
Score:
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     ANDLINE=22388257; PubMed=1247922;

A REDLINE=22388257; PubMed=1247922;

A Lausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsheh F.,

B Actheroto L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Achasten M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rownstein M.J., Worley K.C., Hale S., Garrante P.H.,

A Rohast S., Worley K.C., Hale S., Garrantane P.H.,

A Richards S., Worley K.C., Hale S., Garrantane P.H.,

A Rohast S., Worley K.C., Hale S., Garrante S., Sanchez A.M.,

A Rohast S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

A Rohast S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

B Hakesley B., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

B Rotiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Hones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Buteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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Bernstein P.L., Herrick D.', Prokipcak R.D., Ross J.;
"Control of c-myc mRM half-life in vitro by a protein capable of
binding to a coding region stability determinant.";
                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC051679; AAH51679.1; -.. GG; GO:0003676; F:nucleic acid binding; IEA. InterPro; IPR004087; KH dom. InterPro; IPR004089; KH-type-1. InterPro; IPR005084; KH-type-1.
STRAIN=129/Sv x 129/Sv-CP; TISSUE=Embryonic stem cells;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=129/Sv x 129/Sv-CP; TISSUE=Embryonic stem cells;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 25, Last annotation update)
Coding region determinant binding protein.
IGF2BEL OR CRDBP.
                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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Pfam; PF00016; rrm; 4.
SWART; SW00322; KH; 4.
SWART; SW00360; RRM; 2.
PROSITE; PS50084; KH TYPE 1; 4.
PROSITE; PS50102; RRM; 2.
SEQUENCE 577 AA; 63378 MW; D42
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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STRAIN=C57BH/6J; TISSUB=Embryo;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsudo Y., Nikaido I., Peoole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomica M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Schriml L.M., Subling M., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Ryons P., Rang B., Ringwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Wang K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Nyanahi, Jah.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=94179348; PubMed=8132663;
Prokipeda R.D., Herrick D.U., Ross J.;
Purlification and properties of a protein that binds to the C-terminal coding region of human c-myc mRNA.";
J. Biol. Chem. 269:9261-9269(1994).
                                                                           Herrick D.J., Ross J.; "The half-life of c-myc mRNA in growing and serum-stimulated cells: influence of the coding and 3' untranslated regions and role of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97322234; PubMed=9178888;
Leeds P., Kren B.T., Boylan J.M., Betz N.A., Steer C.J.,
Gruppuso P.A., Ross J.
"Developmental regulation of CRD-BP, an RNA-binding protein that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- SIMILARITY: CONTAINS 4 KH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prokipcak R.D., Leeds P., Doyle G.A.R., Betz N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004087; KH-dom
InterPro; IPR004088; KH-type_1.
InterPro; IPR005094; RNA_rec_mot.
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stabilizes c-myc mRNA in vitro.";
Oncogene 14:1279-1286(1997).
                                             MEDLINE=94158886; PubMed=8114742;
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PROSITE; PS50084; KH TYPE 1; 4.
PROSITE; PS50102; RRM; 2.
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EMBL; AK013940; BAB29071.1; --
HSSP; P11940; 1CVJ.
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                                                                                                                                                                                             ribosome translocation.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fleisig A.J.;
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Query Match: DB:

Best Local

000425;

000425

RESULT 12

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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN-NOD; TISSUE—Thymus;

A MEDLINE=2234683; PubMed=12466851;

The FANTOM CONSORTIUM,

The FANTOM CONSORTIUM,

The RIKEN Genome Exploration Research Group Phase I & II Team;

A the RIKEN Genome Exploration Research Group Phase I & II Team;

The FANTOM CONSORTIUM,

The RICH ACOUST CONSORTIUM,

RE SELL; AKOBB465; BAC40370.1; -.

DR EMBL; AKOBB465; BAC40370.1; -.

DR MGD; MGI: 1890359; Igf2bp3.

CO; GO:0003676; F:nucleic acid binding; IEA.

DR InterPro; IPRO04089; KH-dye_1.

DR InterPro; IPRO04089; KH-dye_1.

DR Fam; PF00013; KH; 4.

DR FAM; PR00015; KH; 4.

DR FAM; PR00322; KH; 4.

SMART; SM00360; RMM; 2.

DR SMART; SM00360; RM TYPE_1; 4.

DR PROSITE; PS50004; KM TYPE_1; 4.

DR PROSITE; PS50002; RMM; 2.

DR PROSITE; PS50002; RMM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Schniml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-UNA-2001 (TrEMBLrel. 17, Created)
01-UNA-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
10 days embryo cDNA, RIKEM full.-length enriched library,
clone:2610036B18, full insert sequence (Igf2 mRNA-binding protein 3)
(Insulin-like growth factor 2, binding protein 3)
Mus musculus (Mouse)
                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63551 MW; 937E601A95D06B77 CRC64;
   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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MEDLINE=21085660; PubMed=11217851;
                                        insulin-like growth factor 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.97e-10
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                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        579 AA;
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Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                  GF2BP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9CPN8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score:
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                                                                                                                                                                                                                  ArgMetValllelleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArgIle 470
                                                                                                                                                                                                                                                     499 AlaGlyArgVallleGlyLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuThr 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, U97188; AAC35208.1; -
EMBL, U7705; AAD39223.1; -
RG); GO:0005737; C:cytoplasm; TAS.
GO; GO:0007737; F:RNA binding; TAS.
GO; GO:0007745; F:RNA binding; TAS.
GO; GO:0007345; F:RNA binding; TAS.
GO; GO:0006412; F:RNA binding; TAS.
GO; GO:0006412; F:RNA binding; TAS.
GO; GO:0006412; F:RNA processing; TAS.
GO; GO:0006412; F:RNA processing; TAS.
InterPro; IPR004089; KH type 1.
InterPro; IPR004089; KH type 1.
InterPro; IPR000408; KH, 4.
Fram; PF000015; KH; 4.
Eram; PF00016; KH; 4.
SMART; SM00320; KH; 4.
FROSITE; PS50084; KH TYPE 1; 4.
PROSITE; PS50084; KH TYPE 1; 4.
PROSITE; PS50003; RRM; 2.
PROSITE; PS00103; RRM; NP 1; FALSE NEG.
SEQUENCE 579 AA; 63720 MW; AESG3A8EE3C135C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mueller-Pillasch F., Lacher U., Wallrapp C.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 4 KH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative RNA binding protein KOC (KOC).
      0000
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
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Mismatches:
Indels:
      Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Mueller-Pillasch F., Lacher U., Wallrapp C.,
Oncogene 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                      579 AA
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Matches:
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                                                                                                                                                       US-09-270-437D-6 (1-3412) x 088477 (1-577)
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19.00
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TISSUE=Pancreas;
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Best Local Similarity:
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Q8C2J9

08C2J9 ID 08 AC 08 DT 01

RESULT 13

q ð

Query Match:

1489 AGGATGATCATCATCACCGGGCCACCGGAAGCCCCAGGTTCAAGGCCCCAGGGACGGATC 1545

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RECORDING FROM N.A.

SEQUENCE FROM N.A.

RECORDING STREL/6; TISSUB-Brain, and Olfactory epithelium;

RECORDINE=22386257; PubMed=1247932;

RADILINE=22386257; PubMed=1247932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Alterni S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Alterni S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Tochiyuki S.C., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

RA BROWNSTEIN M.J., Worden R.J., Abramson R.D., Mullahy S.J.,

RA BROWNSTEIN M.J., Roderian R.J., Lu X., Gibbs R.A.,

RA Norlay K.C., Hale S. Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Nadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.,

RA Generation and initial analysis of more than 15,000 full-length human and mouse couns.
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Shuzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Hyasshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                        Mori H., Sakakibara S., Imai T., Nakamura Y., Iijima T., Suzuki A., Yuasa Y., Takeda M., Okano H.;
"Expression of mouse igf2 mRNA-binding protein 3 and its implications for the developing central nervous system.";
J. Neurosci. Res. 0:0-0(2001).
                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO11689; BAB27779.1; -.
EMBL; AB046173; BAB27779.1; -.
EMBL; BC0496138; AAH45082.1; -.
R EMBL; BC049082; AAH45082.1; -.
R GG; GG:0003676; F:nucleic acid binding; IEA.
R InterPro; IPR004088; KH dom.
R InterPro; IPR004088; KH cype.1.
InterPro; IPR004088; KH cype.1.
InterPro; IPR004088; KH cype.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=Brain, and Olfactory epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63574 MW; CABD9A4355B392B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50084; KH TYPE 1; 4. PROSITE; PS50102; RRM; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and mouse cDNA sequences."
                                                                                                                                                                                                              Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00013; KH; 4.
Pfam; PF00076; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SMO0360; RRM; 2
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SEQUENCE FROM N.A.
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452 ArgMetValllelleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglle 470
                                                                                                                                                                                                                                                   EDUENCE FROM N.A.

Xu C.S., Li W.Q., Li Y.C., Yang K.J., Yan H.M., Chang C.F., Zhao L.F.,
Xu C.S., Li W.Q., Li Y.C., Yang K.J., Wang G.P., Chai L.Q., Yuan J.Y.,
Ma H., Wang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
"Liver regeneration after PH.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY325199; AAP92600.1; -.

ERGUENCE 169 AA; 17743 MW; 19PF6295C1000CBA CRC64;
                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1489 AGGATGGTCATCATCACCGGGCCACCGGAAGCCCAGTTCAAG 1530
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                                                                                                                                                                                                                                                                                                                                                                                                                          ArgMetValIleIleThrGlyProProGluAlaGlnPheLys
                                                                                                                               Last sequence update)
Last annotation update)
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Matches:
Conservative:
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                                                                                    169 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
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                                                                                                                  Created)
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                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                                                                          NCBI_TaxID=10116;
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                                                                                Q7TP50
                                                  RESULT 15
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Search completed: July 16, 2004, 11:29:33 Job time : 183.5 secs

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Matches: Conservative: Mismatches: Indels:

US-09-270-437D-6 (1-3412) x Q9CPN8 (1-579)

Length:

5.97e-10 100.00% 100.00% 1.70%

19.00

Percent Similarity: Best Local Similarity: Query Match:

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BQ691878 AGENCOURT
BM453327 AGENCOURT
BX644668 DKFZp781G
BQ221568 AGENCOURT
                                                                         July 21, 2004, 12:27:22 ; Search time 8233 Seconds (without alignments) 12375.776 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dassa 1 to 874)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: GapDs-rémail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Http://image.llnl.gov

Plate: LLCX2362 row: h column: 03

High quality sequence stop: 653.

874 bp mRNA linear EST 15-JUL-2002 AGNOCORT 8034698 NIH\_MGC\_110 Homo sapiens cDNA clone IMAGE:6207026 Fig. mRNA sequence.

RESULT 1 BQ691878 LOCUS DEFINITION BQ691878.1 GI:21817194 EST. Homo sapiens (human) Homo sapiens

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

151 AGENCOUR. 152 AGENCOUR. 142 AGENCOUR. 142 AGENCOUR. 150 UI - CF - DU. 150 O AGENCOUR. 150 O AGENCOUR. 150 O AGENCOUR. 151 O UI - CF - DU. 152 AGENCOUR. 153 AGENCOUR. 153 AGENCOUR. 153 AGENCOUR. 154 AGENCOUR. 155 AGENCOUR. 155 AGENCOUR. 156 O UI - CF - DU. 157 O AGENCOUR. 156 AGENCOUR. 157 AGENCOUR. 157 AGENCOUR. 157 AGENCOUR. 157 AGENCOUR. 157 AGENCOUR. 157 AGENCOUR. 157 AGENCOUR. 158 AGENCOUR.	BE928277 QV4-CT049 BM462051 AGENCOURT BE896980 601439521 BG254615 602368564
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sapiens cDNA clone IMAGE:5527679
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Average insert size 2 kb. Library constructed by Life
Technologies."
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bisocience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLAM12203 row: e column: 24
High quality sequence stop: 568.
Location/Qualifiers
      721 AGTICTGGATCACCTGTGTATGTCAACAGAAGGGATACCGTCTCCTTGAAGAGGAAACTC
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(Cases 1 to 905)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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6397801 NIH_MGC_72 Homo
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                                                                                                                                                                                                                                                                                                              sapiens (human)
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  Location/Qualifiers
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Best Local Similarity 100.
Matches 834; Conservative
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Homo sapiens cDNA clone IMAGE:6046477
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/lab_host="DH10B"
/clone lib="781 (synonym: hlcc4)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB;
cDNA-collection
                                                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 CCATCTGAGGAATGAGAAGTCTGCGGAGGCGCCAGGGACTCTGCCGAGGCCCTGAGAAC
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                                                                                                                                                                                  1732 GAGGAAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGGCGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         493 AAGCCAAGCAAAAIGCACACCCTITITCIGIGGCAAATCGICICIGIACAGTACGIGIGIGAAA
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0
                                                                                                           Length 832;
                                                                                                                 1.9e-294;
0: Indels
                                                                                                         Score 771; DB 13;
Pred. No. 1.9e-294
                                                                                              22.6%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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AGENCOURT_7559207 NIH_MGC_72
5', mRNA sequence.
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B32 bp mRNA linear EST 04-SEP-2003
DKFZp781G0234_rl 781 (synonym: hlcc4) Homo sapiens cDNA clone
DKFZp781G0234_5', mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 832)

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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dKtz- heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZ)781G0234) is available at the RZPD in Berlin.
Please contact the RZPD Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              721 ATCTCCACCAGCAGGCCCCGCGGAGCTCCCCCCGCTGCCCTACCACCCCTTCACTAC
                                                                                                         361 CATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTGGC
                                                                                                                                                                                                                       ACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAACCC
                                                                                                                                                                                                                                            481 ACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATAAAAACCC
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   TGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTTGAAAT
                     TGTCACCATCCATGCCACCCCCAGAGGGACTTCTGAAGCATGCCGCATGATTCTTGAAAT
                                                                                                                                                541 GGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCGGTGCTGGGGATAGAGAT
                                                                         CATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)
Unpublished (2003)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZP?81G0234"
/dev_stage="adult"
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992

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Fukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

In (Dases 1 to 940)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

CONT Library Preparation: Invitrogen Corp

CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDRM46 row: o column: 04

High quality sequence stop: 695.

Location/Qualifiers
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/mol type="mmNA" |
/mol type="mmNA" |
/db xref="taxon:9606" |
/lab_host="bH10B-Ton A ( Tl and T5 phage resistances) |
/lab_host="bH10B-Ton A ( Tl and T5 phage resistances) |
/lab_host="bH10B-Ton A ( Tl and T5 phage resistances) |
/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site 1: Not1;
Site 2: RecRV (destroyed); Library is oligo-dT primed and directionally cloned (BCoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 22-MAY-2003
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      AGAACTCTGGAGCTGCAGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTG
                                                                   ATTTCCCGCTGCGGATCCTGGTCCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGG
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AGENCOURT 14121251 NIH_MGC_180 Homo sapiens cDNA clone IMAGE:30383283 5', mRNA sequence.
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100.0%; Pred. No. 7.7e-280;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-remail.nih.gov
Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM13292 row: f column: 14
High quality sequence stop: 637.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 5.9e-285;
0; Mismatches 1;
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 DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov column: 05 Plate: NDAMG21 row: e column: 05 High quality sequence stop: 682. Location/Qualifiers
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Best Local Similarity
Matches 715; Conserv
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Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
clissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILL)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                     TAAGGAGCAGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGAGGTGTTGG
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AGENCOURT 15622249 NIH MGC_147 Homo sapiens cDNA clone MAGE:30531076 5', mRNA sequence.
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lypublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.lnl.gov

Plate: LLAM12753 row: a column: 23

High quality sequence stop: 679.

S Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 999)
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/tissue type="duodenal adenocarcinoma, cell line"
/lab host="DHIOB (phage-resistant)"
/lab host="DHIOB (phage-resistant)"
/clone lib="NHI MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length chones and constructed by Life
Technologies. Note: this is a NHI MGC Library."
                                                                 GCCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCCCGGGGAGCAAGGCCACGCCCCTGG
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: ggapbs-r@mail.nih.gov
Tissue Procurement: ArCc
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12276 row: c column: 13
High quality sequence stop: 688.
High quality sequence stop: 688.
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/db xref="taxon:960"
/clone="IMAGE:555552"
/clone="IMAGE:5555552"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 71"
/clone lib="NIH MGC 71"
/slote 2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2:1 kb.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                661 ATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCGGAAAGGAGGGCTTGACCA
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/organism="Homo sapiens"
                                                                                                                                                                                                                                           BM806132.1 GI:19122955
                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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Best Local Similarity 100.
Matches 702; Conservative
                                                                                                                                                                                                                                                                                                      Homo sapiens
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/ Organism="none sapiens"
/ wol type="mRNA"
/ db_xref="taxon:9606"
/ clone="UT-CF-DU1-ads-n-12-0-UI"
/ tissue_type="Primary Lung Epithelial Cells"
/ dev_stage="Adult"
/ lab host="MHIOB (Life Technologies) (T1 phage resistant)"
/ lab host="HIOB (Life Technologies) (T1 phage resistant)"
/ lab host="Ut-CF-DU1"
/ clone lib="Ut-CF-DU1"
/ note="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: Ecok I; Site 2: Not I;
/ UL-CF-DU1 is an ormalized cDNA library containing the following tissue (S: Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lemnon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecok I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) la tail. The sequence tag for this
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                                   Email: paul-mccray@wiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 ACGCCCTGGGGGCACTTCTCAGGCCAGACAGATTGATTTCCCGCTGCGGGATCCTGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG TIŚSUB=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-DUI
TAG_SEQ=GGCTGTAGGC"
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Pred. No. 2e-254;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                             (www.openbiosystems.com)
Seg primer: M13 FORWARD
POLYA=Yes.
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100.0%;
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Tel: 319 356 4866
Fax: 319 356 7171
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                           ATCAAGATTGCCCCTGCGGAAGGCCCCAGACGTCAAGGATGGTCATCATCACCGGG 1509
                                                                                                                                                                                                                                                                                                                                                                                                           CCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAAAC 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TICITIAACCCCAAAGAAGAAGIGAAGCIGGAAGCGCATAICAGAGIGCCCICITCCACA 1629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGA 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAA 1809
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                 ACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCGTTCCCGCAT 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                    CCACCGGAAGCCCGGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAAAC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     652
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1 (bases 1 to 724)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                  113 ACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCGGTTCCCGGCT
                                                                                                                                                                                                             GCCATCATCGGGAAGAGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCT
                                                                                                                                                                                                                                                             GCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 GCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  593 ATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCAAGATCAGGGAAATTGTACAA
                                                                                                                                                             173 CATCACTOTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAGACCAAACGCAGCCAGCCAGATCGGGAGCAAACCA 1967
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MCCTAY Lab University of Iowa Med Labs, Iowa City, IA 52242, USA 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
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I (bases 1 to 647)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                              541 TITATCICCCCCCCCCCCCCCCCTTCTTCTCTCCATCTTTTGAATTTCCTC
                                   TGTTAAGATATGTGGCCTGTGGGTTACACGGGTGCCTGCAGCGGTAATATTTTAGAA
                                                                                                                     TTTTAAAGAGAAAGCAGGCTTTTCTAGACTTTAAAGAATAAAGTCTTTGGGAGGTCTCTCAC
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836 bp mRNA linear EST 02-MAY-2002
AGENCOURT_7675661 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6095809
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/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/lab host="Th1 MGC 72"
/note="Torgan: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1368 row: n column: 02
High quality sequence stop: 670.
Location/Qualifiers
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases 1 to 836)
II (Mage.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                  TCATGCAGAAAGAGGCAGATGAGCCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTGG
                                                                                                                                                                                      554 CACACAATGGCTTGGTTGGAAGACTGATTGGAAAGAAGGCAGAAATTTGAAGAAAATTG
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                                                                         TCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTGG
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.larity 100.0%; Pred. No. 2.2e-243;
Conservative 0; Mismatches 0; Indels
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:6095809"
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BG748346 889 bp mRNA linear EST 15-MAY-2001
602705902F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4842553 5',
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/lab host="DH10B (phage-resistant)"
/clone_lib="NNH_MGC-43"
/note="Organ: eye; Vector: poTB7; Site_1: Xho1; Site_2:
Clone_lib="NNH made by oligo-dT priming. Directionally—
cloned into EcoRI/Kho1 sites using the following 5;
adaptor: GGCAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of
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I (bases 1 to 889)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library. |"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can J found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCNL677 row: c column: 02
High quality sequence stop: 773.
Location/Qualifiers
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Best Local Similarity 99.7%; Pred. No. 1.7e-233;
Matches 717; Conservative 0; Mismatches 2;
                                  971 AACATGAAACAGGGACCAAGATAACAATCTCATC 1004
                                                                       614 AACATGAAACAGGGACCAAGATAACAATCTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .889
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:4842553"
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BG748346.1 GI:14058999
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                                                                                                                                                                                                                                                                                                               /done libe unit control of the recombination of the property of the following forcer: property of the following with a modified polylinker; Site_1: EcoR I; Site_2: Not I; UT-CF-DUO is a cDNA library containing the following tissue(8): Primary Lung Epithelial Cells The library was constructed according to Bonaldo, Lemnon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA Synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the communication of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCCCCTTCGCCCCCCCCAGCGAGCCCAGCGTGGGGACCACTCTTCCCGGGAGCAAGGCC 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAAATTG 970
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TAG_LIB=UI-CF-DUO
TAG_SEQ=GGCTGTAGGC"
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0
                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-DU0-aac-j-06-0-UI"
/tissue_type="primary Lung Epithelial Cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.6%; Score 634; DB 13; Length 647;
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                                                                                                                                                                                                                                                         /dev stage="Adult"
/lab_host="DH10B (Life Technologies)
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AGENCOURT 7965128 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6162660
5', mRNA sequence.
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1 (bases 1 to 894)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                 1845 AGTCGCCTCACAGCGCAGCAAGTGAGGCTCCCACAGGCACCAGCAAACAACGATGAAT
                                                                                                                                                                                                                    TGAGAACCCCAGGGGCCGAGGAGGGGGGGGGGAAGGTCAGCCAGGTTTGCCAGAACCACC
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                                             17.4%; Score 594; DB 12;
99.7%; Pred. No. 2.3e-224;
live 0; Mismatches 2;
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                                             Query Match
Best Local Similarity 99.7
Matches 694; Conservative
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El (Lases I to 781)

In (Lases I to 781)

NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rømail.nih.gov

Tissue Procurement: DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Location/Operation of the Colour of the Colour of the Colour of the Colour of the Colour of the Colour of the Colour of the Colour of the Colour of the Colour of the Colour of the Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of Colour of C
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CGCCCCTGGGGGGCACTTCTCAGGCCAGACAGATTGATTTCCCGCTGCGGATCCTGGTCCC
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BQ212353.1 GI:20392498
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ilarity 99.8%;
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                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/tissue_type="melanotic melanoma"
/lab_host="DHIOB (phage-resistant)"
/clone_lib="NHI MGC 72"
/note="Organ: Skin" Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.lnh.gov
Plate: LiaMi3516 row: Column: 13
High quality sequence stop: 666.
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99.8%; Pred. No. 8.1e-223;
iive 0; Mismatches 1;
Procurement: ATCC/DCTD/DTP
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/tissue Lype="melanotic melanoma"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT Average libeart size 2 kb. Library constructed by Life
Technologies."
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MG clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13335 row: a column: 01
High quality sequence stop: 590.
Location/Qualifiers
                                                                                                                                                                           Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I MASSS 1 to 918)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (Unpublished (1999)
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Pred. No. 7.6e-221;
0; Mismatches 1;
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Tissue Procurement: ATCC/DCTD/DTP
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Page

20; SEQ ID NO 37153; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this placent did not appear in the printed specification, but was obtained in the contract of the contr ftp.wipo.int/pub/published\_pct\_sequences

Sequence 614 AA

euTyrIleGlyAsnLeuSerProAlaValThrAlaAspAspLeuArgGlnLeuPheGlyA yrGlyThrValGluAsnValGluGlnValAsnThrAspThrGluThrAlaValValAsnV TTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACCTCCGGCAGCTCTTTGGGG ACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTGAAGTCCGGGCTACGCCTTCGTGGACT SparglysleuProleuAlaGlyGlnValLeuLeuLysSerGlyTyrAlaPheValAspT isGlyLys11eMetGluValAspTyrSerValSerLysLysLysLeuArgSerArgLysIleG heGluAsnTyrSerPheLysIleSerTyrIleProAspGluGluValSerSerProSerP GCCGGGTACCGGGCCGGGGGCTCTCGGGGAAGAGACGATGATGAACAAGC ACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGTAAAGTGGAATTGC ATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAGGAGCAGGAAAATTC TCACATATGCAACAAGAGAAGAAGCAAAAATAGCCATGGAGAAGCTAAGCGGGCATCAGT alThrTyrAlaThrArgGluGluAlaLysIleAlaMetGluLysLeuSerGlyHisGlnP TTGAGAACTACTCCTTCCAAGATTTCCTACATCCCGGATGAAGAGGTGAGCTCCCCTTCGC 614 610 0 2 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: (1-614)US-09-270-437D-6 (1-3412) x ABG06794 5.53e-271 3094.00 99.03% 99.03% 50.55% Best Local Similarity: Score: Percent Similarity: Alignment Scores: 09 80 Н 20 143 40 100 120 23 83 203 263 323 383 443 140 503 Query Match: DB: ð q δ g 8 qq qq ð  $\delta$ g g à g à ğ g ð

142

82 20 40

202

09

262

80

322 100 382

120

442 140 502 562 180

160

Db

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1102 1162 1582 1222 1282 1342 1402 1462 1642 1042 1522 360 622 200 682 220 742 240 802 260 862 922 300 982 320 340 380 400 420 440 460 480 500 520 540 euValdJyArgLeuIleGlyLysGluGlyArgAsnLeuLysLysIleGluHisGluThrG roProGlnArgAlaGlnArgGlyAspHisSerSerArgGluGlnGlyHisAlaProGlyG TTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACTAAGCAGACCCCAGT alGlyAlaIleIleGlyLySGluGlyLeuThrIleLySAsnIleThrLySGlnThrGlnS CCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAGCCTGTCACCATCC erArgValAspIleHisArgLysGluAsnSerGlyAlaAlaGluLysProValThrIleH ATGCCACCCCAGAGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATCATGCAGAAAG AGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTGGCACACAATGGCT luAlaAspGluThrLysLeuAlaGluGluIleProLeuLysIleLeuAlaHisAsnGlyL TGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAAAATTTGAAACAG GGACCAAGATAACAATCTCATCTTTGCAGGATTTTGAGCATATACAACCCGGAAAGAACCA TCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAGATAGAGGATTATGAAGAAGC TGCGTGAGGCCTTTGAAAATGATATGCTGGCTGTTAACCAACAAGCCAATCTGATCCCAG euArgGluAlaPheGluAsnAspMetLeuAlaValAsnGlnGlnAlaAsnLeuIleProG GGTTGAACCTCAGCGCACTTGGCATCTTTTCAACAGGACTGTCCGTGCTATCTCCACCAG CAGGGCCCCGCGGAGCTCCCCCCCCGCTGCCCCTACCACCCCTTCACTACCCACTCCGGAT ACTICICCAGCCIGIACCCCCATCACCAGITITGGCCCCGTTCCCCGCATCATCACTTATC 420 yrPheSerSerLeuTyrProHisHisGlnPheGlyProPheProHisHisSerTyrP CAGAGCAGGAGATTGTGAATCTTCATCCCCAACCCAGGCTGTGGGCCCCATCATCGGGA AGAAGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAGATTGCCC ysLysGlyAlaHisIleLysGlnLeuAlaArgPheAlaGlyAlaSerIleLysIleAlaP CTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAAGCCC roAlaGluGlyProAspValSerGluArgMetVallleIleThrGlyProProGluAlaG AGTICAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAAACTTCTTTAACCCCA 500 lnPheLysAlaGlnGlyArgIlePheGlyLysLeuLysGluGluAsnPhePheAsnProL AAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCTGGCCGGGTGA 520 ysGluGluValLysLeuGluAlaHisIleArgValProSerSerThrAlaGlyArgVall 743 280 340 360 380 400 460 480 180 200 220 240 803 260 300 1043 1103 1343 1403 683 863 923 1223 1283 1463 1523 623 983 1163 g 임 qq 셤 à g g à d  $\delta$ ΩD ð g ŏ g ŏ gg OD Db ò à à ò à ò ò 셤 ð q à Š

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TTGGCAAAGGTGGCAAGACCGTGAACGAACTGCAGAACTTAACCAGTGCAGAAGTCATCG 1702
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                                                                        hePheAlaSerGlnThrAlaGlnArgLysIleArgGluIleValGlnGlnValLysGlnG
                                                                                                                                                            TCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAACAGGTGAAGCAGC
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Claim 11; SEQ ID NO 1116; 980pp; English.
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                                                                Rosen CA,
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New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a lead of pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (EBISA) Disorders with the disorders and in diagnostic immunoassays e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, ortuses and fungi and ocular disoaders e.g. corneal infection, bacteria, viruses and fungi and ocular disoaders e.g. corneal infection, can many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, cor regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed

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cardiovascular disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.

New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or respiratory, rep renal disorders.

Claim 11; SEQ ID NO 1116; 402pp; English.

The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. system, clupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. and multiple sclerosis), muscular disorders, respiratory diseases (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left chart syndrome), renal disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left chart syndrome), renal disorders (e.g. equite kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and spendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial inflamatory diseases. Sequences ABUS5499 and MUS5748 represent human novel polypeptides of the invention 

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CACCATCCATGCCACCCCAGA( 
TGCAGAAGGCAGATGAGAC 
CAATGGCTTGGTTGGAAGACTGATT 
TGAAACAGGGACCAAGA: 
AAGAACCATCACTGTGAAGGG( 
TGAAGAAGCTGCGTGAGG( 
GATCCCAGGGTTGAACCT
CTCCACCAGCAGGCCC
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CTCTTATCCAGAGCAGGAGA 
CATCGGGAAGAAGGGG 
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543 GlyArgValIleGlyLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuThrSerAla 562
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                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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| IleLeuAlaHisAsnGlyLeuValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLys
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                               AAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTTGAGCATA
                                                        Lys1leGluHisGluThrGlyThrLys1leThr1leSerSerLeuGlnAspLeuSerIle
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central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
                                                                                                                                                                                                                                                                                          Kovatis SG;
                                             familial history;
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Zhao X,
                           Human ovarian cancer marker M452
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14-MAR-2001; 2001US-0276025P.
10-AUG-2001; 2001US-0313132P.
19-SEP-2001; 2001US-0323860P.
26-SEP-2001; 2001US-0324967P.
26-SEP-2001; 2001US-0324967P.
26-SEP-2001; 2001US-0325499P.
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Meyers RE, Morrisey MP, O
        (first entry)
                                               cancer;
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N-PSDB; ABS76442.
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                                                                                                                       Homo sapiens.
        11-DEC-2002
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Assessing whether a patient is afflicted with ovarian cancer, useful ir assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.

Disclosure; Page 263-264; 481pp; English.

The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression level of a marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing cancer (e.g. patients having a familial history of ovarian cancer. The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzheimer's disease or Parkinson's disease), brain disorders (e.g. bacterial or viral meningitis or encephalitis), inflammations (e.g. bacterial or viral meningitis or encephalitis), testicular disorders (e.g. nontuberculous granulomatons orbitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with ovarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, selecting a composition for inhibiting ovarian cancer, assessing the ovarian carcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present amino acid sequence represents one of the ovarian cancer markers described in the invention

Sequence 556 AA;

ABG96346 standard; protein; 556 AA

ABG96346;

AAAATCATATGCTGGCTGTTAACCAACAAGCC 1149 ACGCCAGATGAAAATGAGGAAGTGATCGTCAGA 1749 CAGTIGAGGCCTGTGCCAGTGCTGAGATAGAG 1089 ACCCCCATCACCAGITIGGCCCGITCCCGCAT 1329 ANGTCAGCGAAAGGATGGTCATCATCACCGGG 1509 TGGAAGCGCATATCAGAGTGCCCTCTTCCACA 1629 CTCCCCCCCCTGCCCCTACCACCCCTTCACT 1269 TCAAACAGCTGGCGAGATTCGCCGGAGCCTCT 1449 AGACCGTGAACGAACTGCAGAACTTAACCAGT 1689 hrvalglualacysalaseralagluileglu 340 CACTIGGCALCTITICAACAGGACTGICCGIG 1209 357 leSerSerLeuGlnAspLeuSerIleTyrAsn 320 CCTCAGGGAGTCGCCTCACAGCGCAGCAAG 1866 K3-Antagonist; cancer; NOV.

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                                                              ProValThrMetHisAlaThrProGluGlyThrSerGluAlaCySArgMetIleLeuGlu
             GCACACAATGGCTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAATT
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                                                                                                                                                                                                                                                                                                                                                                treating
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                                        05-OCT-2001; 2001US-0327454P.
09-OCT-2001; 2001US-0328029P.
09-OCT-2001; 2001US-0328029P.
12-OCT-2001; 2001US-0328845P.
15-OCT-2001; 2001US-0329845P.
17-OCT-2001; 2001US-0349414P.
17-OCT-2001; 2001US-034957P.
22-OCT-2001; 2001US-034957FP.
01-NOV-2001; 2001US-034957FP.
01-NOV-2001; 2001US-034957FP.
01-OCT-2002; 2002US-0391342P.
01-OCT-2002; 2002US-0391342P.
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N-PSDB; ACA90176.
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Best Local Similarity:
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 ATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGG 1509
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                                                                                                                                                                                              The present sequence represents a murine c-myc coding region determinant binding protein (CRD-BP). The presence or absence of a tumor can be determined by determining the levels of CRD-BP present in the suspect tissue, where the CRD-BP shields c-myc RNA from endonucleolytic attack and so prolongs its half-life. The methods are used for diagnosing presence or absence of a tumor in a human, especially breast, colon and pancreatic cancer. They are also used to inhibit cancer cell growth
                                                                                                                                                                                                                                                                          CAGGIGAAGCAGCAGAGAAAIACCCICAGGGAGICGCCICACAGCGCAGCAAG 1866
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N-PSDB; AAZ10617.
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                        Conservative:
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Matches:
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This invention describes a novel isolated polypeptide (1) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polynucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention data be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the different time points. CD4+ and/or CD8+ T-Cells isolated from a patient are tracted with P2, polynucleotides encoding P2 or antigen presenting cells expressing P2 and then administered to the patient to inhibit
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17-DEC-1999; 99US-0046596.
30-DEC-1999; 99US-0046496.
10-JAN-2000; 2000US-00480894.
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  vaccine; detection
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The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions
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                                                                                                                                                                                                                                                                                                                                tumour; lung cancer; cytostatic; immunostimulant; vaccine;
1501 ATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAA
                                                                   IleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglleTyrGlyLvSIleLys
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Retter MW, Marnerakis M,
Watanabe Y, Peckham DW;
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PD, Fanger N, Rette
FS, Carter D, Watan
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CC comprising the lung tumour proteins, polynucleotides, antibodies, fusion
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<b>388888</b>	comprising the 1 proteins, T cell the lung tumour stimulating an i ABB75070 represe invention	ng the lun T cell p tumour pr ing an imm represent	(the lung tumour proteins, I T cell populations, or anti umour proteins are useful f gg an immune response. ABLA8 epresent sequences used in	ins, polynucleot antigen present ful for treating ABL48959 to ABL4 d in the exempli	polynucleotides, antibodies, fusion iden presenting cells that express for treating lung cancer or 8959 to ABL49300 and ABB74946 to the exemplification of the present
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δλ	73	ATGAACAAG	ATGAACAAGCTTTACATCGGGAA	CCTGAGCCCCGCCGTC	CGGGAACCTGAGCCCCGCCGTCACCGCCGACGACGCTCCGGCAG 132
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ठे ह	133	CTCTTTGGG	GACAGGAAGCTGCC	ccreeceseacassrc  ::::::     valenter	⊣ •
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qq	61	:::      IleGluLeu	:::	:       :::::     eGluValGluHisSer	 erValProLysArgGlnArgIle 80
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ò	373	TIGGCTCAA	TATGGGACAGTGGA	BAATGTGGAACAAGTC	TIGGCICAATAIGGGACAGIGGAGAAIGIGGAACAAGICAACACAGACACAGAACGGCC 432
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gg	21	ValValAsn'	ValThrTyrSerSe	rLysAspGlnAlaArg	GlnAlaLeuAspLysLeuAsn 140
ð f	493	GGGCATCAG	TTTGAGAACTACTC	CTTCAAGATTTCCTAC	55
₹ 8	53	TCCCCTTCGCCC	cccctcag	Leunysvalalyr -CGAGCCCAGCGT	.lerroAspeluintAlaAla 160 GGGGACCACTCTTCCCGG 600
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λŏ	601	GAGCAAGGCC	CACGCCCTGGGGG	CACTTCTCAGGCCAGA	CACGCCCTGGGGGCACTTCTCAGGCCAGACAGATTGATTTCCCGCTGCGG 660
Op	181	ArgGlnGly	SerProGlySe	rValSerLysGlnLys	   ProCysAspLeuProLeuArg 199
ογ	661	TCCTGGTC	CCCACCCAGTTGTTGGTGCCATCAT	rggrgccarcarcgga	CGGAAAGGAGGCTTGACCATAAAG 720
g	200	LeuLeuVall	ProThrGlnPheva		LysGluGlyAlaThrIleArg 219
δy	721	AACATCACT	AAGCAGACCCAGTC	CACTAAGCAGACCCAGTCCCGGGTAGATATCCAT;	CATAGAAAGAGAACTCTGGAGCT 780
QQ	220	AsnileThr	LysGlnThrGlnSe	LysileAspvalHis	ArgiysGluAsnAlaGlyAla 239
À i	781	GCAGAGAAG	GCAGAGGCTGTCACCATCCATGCCAC		4
q	240	AlaGluLys	SerileThrileLeu	ıSerThrProGluGly'	ThrSerAlaAlaCysLysSer 259
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                                                                                                                                                                                                                                                                                                                                                                    The present invention describes human lung tumour proteins. Human lung activities, and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABD74946 to ABB75070 represent sequences used in the exemplification of the present
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Fanger GR;
                              tumour; lung cancer; cytostatic; immunostimulant;
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         L523S protein sequence SEQ ID NO:348
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Retter MW, Marnerakis M,
Watanabe Y, Peckham DW;
                                                                                                                                                                                                                                                                                                                      polypeptides,
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Conservative:
Mismatches:
Indels:
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lung cancer or stimulating an immune response.
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PD, Fanger N, Retter
TS, Carter D, Watanab
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                     The present invention describes human lung tumour proteins. Human lung actions and polymucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
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                                                                                                                                      lung tumour; lung cancer; cytostatic; immunostimulant; vaccine;
                                         GGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGGGAAGGATGGTCATC
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                                                                                                                                                                                                                                                             Polynucleotides encoding lung tumor polypeptides, useful for treating lung cancer or stimulating an immune response.
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Carter D, Watanabe Y,
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The present invention describes isolated human lung carcinoma polypeptides (II) (I) and (II) have cytostatic polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by cobtaining a biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide to a cancer in comparing the amount of polynucleotide that hybridises to the oligonucleotide to a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ32145 to ABQ32466 and ABBPG1866 to ABBPG1802 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAACAAGCTTTACATCGGGAACCTGAGCCCCCGCCGTCACCGCCGACGACCTCCGGCAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                    TS;
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                                                                                                                                   fiuman; lung cancer; lung tumour; cytostatic; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                  Henderson RA;
nger GR, Vedvick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel lung carcinoma polynucleotide sequences and polypeptides encorthe polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.
                                                                                                  Human lung cancer associated protein sequence SEQ ID NO:348.
                                                                                                                                                                                                                                                                                                                                                                                                                 X, Kalos MD, Hendersor
Durham M, Fanger GR,
Cai F, Foy IM;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Wang T, Wang A, Skeiky YAW, Li SX
Mcneill PD, Fanger N, Retter MW,
Carter D, Watanabe Y, Peckham DW,
                                                                                                                                                                                                                                                                                                          12-DEC-2000; 2000US-00735705.
07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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1957.50
79.19%
65.48%
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                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABQ92440,
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Mcneill E
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RESULT 12 ABP61917

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                        GTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAGGAGC
                                                                         TTGCCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACACAGACACAGAAAACCGCC
                                                                                                  GTTGTCAACGTCACATATGCAACAAGAAGAAGCAAAAATAGCCATGGAGAAGCTAAGC
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397 TyrProGlnPheGluGln---SerGluThrValHisLeuPheIleProAlaLeu
                                                                                                                                                                                      496 SerPhealaaladlyAxgVallleGlyLysGlyGlyLysThrValasnGluLeuGlnAsn
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Retter MW, Durham M, Fanger GR, Vedv
Peckham DW, Cai F, Foy TM;
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--SerGlyProProSerAlaMetThrPro-
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PD, Fanger N, Retter
), Watanabe Y, Peckhā
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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N-PSDB; ABQ92485.
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Novel lung carcinoma polynucleotide sequences and polypeptides encoded by the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.

Page 375-377; 381pp; English Claim 9; The present invention describes isolated human lung carcinoma polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic cativity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of cample with the oligonucleotide that hybridises to the oligonucleotide to a mount of polynucleotide that hybridises to the oligonucleotide to a cancer in a patient. (I) and (II) are useful in pharmaceutical compositions, e.g. the patient. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABP621945 to ABP61866 to the patient sequences used in the exemplification of the present invention

Sequence 579 AA;

CTCTTTGGGGACAGGAAGCTGCCCCTGGCGGACAGGTCCTGCTGAAGTCCGGCTACGCC 192 GIGGAATIGCAIGGGAAAICAIGGAAGTIGAITACICAGICICIAAAAAGCIAAGGAGC 312 GTTGTCAACGTCACATATGCAACAAGAAGAAGAAGCAAAAATAGCCATGGAGAAGCTAAGC 492 TCCCCTTCGCCCCCTCAG-----CGAGCCCAGCGT-----GGGGACCACTCTTCCCGG 600 ATGAACAAGCITTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTCCGGCAG 132 TTCGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCCATCGAGACCCTCTCGGGTAAA MetAsnLysLeuTyrIleGlyAsnLeuSerGluAsnAlaAlaProSerAspLeuGluSer TTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACACAGACACAGAAACCGCC GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGC 579 381 81 94 29 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: (1-579)US-09-270-437D-6 (1-3412) x ABP61974 6.18e-168 1957.50 79.19% 65.48% Percent Similarity: Best Local Similarity: gnment Scores: 161 73 133 21 193 41 253 61 313 121 141 553 601 81 373 101 433 493 Query Match: DB: .. No.: d ò q qq 96 AS ₹ 셤 à à ð g 8 염 8 g à

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qa	181	ArgGlnGlySerProGlySerValSerLysGlnLysProCysAspLeuProLeuArg 199
Qy	661	
DP	200	eubeuvalProThrGlnPheValGlyAlaIleIleGlyLySGluGlyAlaThrIleAr
ζ	721	CATAGAAAAGAGAACTCT
ДQ	220	
٥y	781	GGGACTTCTGAAGCATGCCG
qq	240	AlaGluiysSerIleThrileLeuSerThrProGluGlyThrSerAlaAlaCysLysSer 259
ζ	841	ATTCTTGAAATCATGCAGAAAGAGGGAGAGAGACAAACTAGCCGAAGAGATTCCTCTG 900
qq	260	ileLeuGluileMetHisLysGluAlaGlnAspileLysPheThrGluGluileProLeu 279
δ	901	TG 96
qq	280	LysīleLeuAlaHisAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeu 299
ργ	961	ABABAAATIGAACATGAAACGGGCGACGAAGATAACAATCTCATCTTTGCAGGATTTGAGC 1020
qa	300	LyslyslleGluGlnAspThrAspThrLyslleThrIleSerProLeuGlnGluLeuThr 319
δλ	1021	ATATACAACCGGGAAAGAACCATCACTGTGAAGGCACAGTTGAGGCCCTGTGCCAGTGCT 1080
qq	320	LeulyrAsnProGluArgThrIleThrValLysGlyAsnValGluThrCysAlaLysAla 339
Qy	1081	SAGATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGTTAAC 1140
qa	340	31uGluGluIleMetLysLysIleArgGluSerTyrGluAsnAspIleAlaSerMetAsn 359
<i>\</i> 0	1141	CAACAAGCCAATCTGATCCCAGGGTTGAACCTCAGCGCACTTGGCATCTTTTCAACAGGA 1200
qa	360	LeuGlnAlaHisteulleProGlyLeuAsnLeuAsnAlaLeuGlyLeuPhe 376
ο,	1201	CTGTCCGTGCTATCTCCACCAGGAGGCCCCGGGAGCTCCCCCGGCTGCCCCTACCAC 1260
Dp	377	
λ	1261	CCCTTCACTACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCG 1320
QQ	387	
ογ	1321	321 TICCGGCATCATCACTCTTATCCAGAGAGAGATTGTGAATCTCTTCATCCCAACCCAG 1380
ρp	397	IyreroglnPhegluglnSergluThrdluThrValHisLeuPheileProAlaLeu 415
ζ	1381	GCTGTGGGCGCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCC 1440
Dp	16	
ò	H	BATGGTCATC 15
Dþ	436	lyAlaSerileLysileAlaProAlaGluAlaProAspAlaLysValArgMetValil
δγ	1501	TTTGGGAAACTGAAA 15
අග	99	leThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglleTyrGlyLysIl
ζ	н	GGAAAACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGC
Db	92	
ò	-	CGAACTGCAGAAC 16
Db	96	erPheAlaAlaGlyArgVallleGlyLysGlyGlyLysThrValAsnGluLeuGlnAsn
ò	81	AAATGAGGAAGTG 17
qq	16	euSerSerAlaGluValValValProArgAspGlnThrProAspGluAsnAspGlnVal 53

192

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120 492 140 552 160 009 180

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AAGAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCTCATCTTTGCAGGATTTGAGC 1020
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181 ArgGinGly---SerProGlySerValSerLysGlnLysProCysAspLeuProLeuArg
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             1741 ATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAA 1800
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nger GR, Vedvick TS;
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M. Fanger GR,
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W, Cai F, Foy TM;
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Retter MW, I
Peckham DW,
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07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
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Mcneill PD, Fanger N, Rette
Carter D, Watanabe Y, Peckh
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                                                                                                                                                                    ABP61973 standard; protein;
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                       CAACAAGCCAATCTGATCCCAGGGTTGAACCTCAGCGCACTTGGCATCTTTCAACAGGA 1200
                                                    1201 CTGTCCGTGCTATCTCCACCAGCAGGCCCCGGGAGCTCCCCCCGGCTGCCCCTACCAC 1260
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TyrProGlnPheGluGln---SerGluThrGluThrValHisLeuPheIleProAlaLeu 415
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                                 360 LeuGlnAlaHisLeuIleProGlyLeuAsnLeuAsnAlaLeuGlyLeuPhe
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ATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTCCGGCAG 132
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nger GR, Vedvick TS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang T, Wang A, Skeiky YAW, Li SX, Kalos MD, Henderso
Mcneill PD, Fanger N, Retter MW, Durham M, Fanger GR,
Carter D, Watanabe Y, Peckham DW, Cai F, Foy IM;
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980S-00123912.

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12-DEC-2000;
07-MAY-2001;
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:::	TTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACACAGAACAGGAAACCGCC 432 	GTTGTCAACGTCACATATGCAACAAGAAGAAGAAGACAAAAATAGCCATGGAGAAGCTAAGC 492 	GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGGATGAAGAGGTGAGC 552	TCCCCTTCGCCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTCCGG 600 :::	GAGCAAGGCCACGCCCTGGGGGACTTCTCAGGCCAGACAGA	ATCTGGTCCCCACCCGTTTGTTGGTGCCATCATCGGAAAGGAGGCTTGACCATAAAG 720 :::	AACATCACTAAGGAGCCGAGTCCCGGGTAGATATCCATAGAAAGAGAACTCTGGAGCT 780	GGAGAGAGACTGTCACCATGCACCCCAGAGGGACTTCTGAAGCATGCGGCATG 840	ATTCTTGAAATCATGCAGAAAGAGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTG 900	AAAAICTIGGCACACAAIGGCIIGGIIGGAAGACIGAIIGGAAAAAGAAGGAGAAAITIG 960 	AAGAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGGAGC 1020                :::	AINTACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCT 1080 :::	GAGATAGAGATTATGAAGAGAGAGCTTTGAAAATGATATGCTGGTGTTAAC 1140	CAACAAGCCAATCTGATCCCAGGGTTGAACCTCAGGCACTTGGCATCTTTTCAACAGGA 1200	CTGTCCGTGCTATCTCCACCAGCAGGACCCCGCGGAGCTCCCCCGCTGCCCC 1260	CCCTTCACTACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCG 1320	TTCCCGCATCATCACTTATCCAGAGAGATGTGTGAATCTCTTCATCCAACCCAG 1380 :::	GCTGTGGGCGCCATCATCGGGAGAGAGGGCGCACACAAACAGCTGGCGAGATTCGCC 1440
 81 ArgLys	373 TTGGCT     101 LeuVal	433 GTTGTC        121 ValVal	493 GGGCAT     141 GlyPhe	553 TCCCCT	601 GAGCAAGGC        181 ArgGlnGly	661 ATCCTG :::    200 LeuLeu	721 AACATC        220 AsnIle	781 GCAGAG        240 AlaGlu	841 ATTCTT        260 IleLeu	901 AAAATC        280 Lysile	961 AAGAAA        300 LysLys	1021 ATATAC :::    320 LeuTyr	1081 GAGATA      340 GluGlu	1141 CAACAA      360 LeuGln	1201 CTGTCC 377	1261 CCCTTC 387	1321 TTCCCG :::    397 TYrPro	1381 GCTGTG :::

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Search completed: July 16, 2004, 10:38:50 Job time : 191 secs

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US-09-261-855-2
; Sequence 2, Application US/09261855A
; Sequence 2, Application US/09261855A
; Patent No. 6255055
; GENERAL INFORMATION:
; APPLICAMT: ROSS, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/261,855A
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 577
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27980, A
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28001, A
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US-09-261-855-12

US-09-261-855-21

US-09-261-855-21

US-09-261-855-21

US-09-261-855-17

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Best Local Similarity:
   Alignment Scores:
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US-09-481-897-176
US-09-481-84A-176
US-09-482-842-615A-176
US-09-606-421B-176
US-09-506-421B-176
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                  AAGAAAATTGAACATGAAACAGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGC
                                                          GCTGTGGGGCGCCATCATCGGGAAGAAGAGGGCACACAACAACAGCTGGCGAGATTCGCC
       AAAATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTG
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
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Best Local Similarity:
Query Match:
        ; SOFTWARE: FastSE
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo s
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          APPLICANT: Hosken, Mancy
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Los Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITION AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45509
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOSTWARE: FastSEQ for Windows Version 3.0
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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ORGANISM: Homo sapiens
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APPLICANT: Rang, insughable
APPLICANT: Ralos, Michael D.
APPLICANT: Bengur, Chaitanya S.
APPLICANT: Bengur, Chaitanya S.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Wang, Aljun A.
APPLICANT: Wang, Aljun A.
APPLICANT: Menderson, Robert A.
APPLICANT: Moneill, Particia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
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Mismatches:
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Length:
Matches:
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US-09-643-597-176
Sequence 176, Application US/09643597
; Patent No. 6426072
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Fan, Ligun
Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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APPLICANT: Wang, T
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OY 1621 TCTTCCACAGCTGGCTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC	Oy 1801 ATTGTACAACAGGTGAAGCAGCAGAAAA 1833    -::	; Sequence 176, Application US/09480884A; Sequence 176, Application US/09480884A; Patent No. 6482597; GENERAL INFORMATION: ; APPLICANT: Wang, Tongtong; APPLICANT: Fan, Liqun; APPLICANT: Hosken, Nancy A.; APPLICANT: Kalos, Michael D.	; APPLICANT: Fanger, Gary R.; ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER; FILE REFERENCE: 210121.455C6; CURRENT APPLICATION NUMBER: US/09/480, 884A; NUMBER OF SEQ ID NOS: 330	<ul> <li>SOFTWARE: FastSEQ for Windows Version 3.0</li> <li>SEQ ID NO 176</li> <li>IENGTH: 579</li> <li>TYPE: PRT</li> <li>ORGANISM: Homo sapiens</li> <li>US-09-480-884A-176</li> </ul>	Gument Scores:  1.69e-164 re: 1950.50 cent Similarity: 79.02\$ rt Local Similarity: 65.31\$ ry Match:	Gaps: 8   8   9   9   9   9   9   9   9   9	н		Oy 253 GTGAAATTGCATGGGAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAGGAGC 312  Db 61 11eGlubeuHisGlyLysProlleGluvalGluHisServalProLysArgGlnArglle 80  Oy 313 AGGAAAATTCAGAACATCCCTCCTCACCTGCAGGGAGGTGTTGGACTT 372  Db 81 ArdlysLanGlyLlaargaachtlong	

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Sequence 176, Application US/09542615A
Patent No. 6518256
GENERAL INFORMATION:
APPLICANT: Wand Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Fance Content S.
APPLICANT: Fance Content S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAE;
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER;
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER;
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
SUGFRMARE: FastSEQ for Windows Version 3.0
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-09-542-615A-176
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APPLICANT: Fan, ALMSCLESS
APPLICANT: Fan, Lingun
APPLICANT: Fan, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Mancy
APPLICANT: Hosken, Mancy
APPLICANT: Hosken, Mancy
APPLICANT: Mang, Aliun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: 201021.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 579
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Matches:
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Mismatches:
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Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
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Best Local Similarity:
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US-09-606-421B-176
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US-09-606-421B-176
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ORGANISM:
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97 rArgSerVal---MetThrGluGluTyrLysValProAspGlyMetValGlyPhellell
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Matches:
Conservative:
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Indels:
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NAME: WILLIAM S. FELLEAR
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-480
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644
STRANDEDNESS: SINGle
STRANDEDNESS: SINGle
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
TOPOLOGY: Unknown
TOPOLOGY: Unknown
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                                                                                                                                                                          TOPOLOGY: Unknown MOLECULE TYPE: Peptide/Protein HYPOTHETICAL: No ORIGINAL SOURCE:
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245.00
35.64%
22.76%
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                                                  1261 CCCTTCACTACCCACTCCGGATACTTCTCCAGCCTGTACCCCCCATCACCAGTTTGGCCCG 1320
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; Sequence 2, Application US/08021608D
; Patent No. 5580760
; GRERAL INFORMATION:
    APPLICANT: LEVENS, DAVID L., DUNCAN,
    APPLICANT: ROBERT C., AND AVIGAN, MARK I.
    TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR NUMBER OF SEQUENCES. 24
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: MORGAN & FINNEGAN
    STREET: MORGAN & FINNEGAN
    STREET: MEW YORK
    COUNTRY: USA
                                                                                         -SerGlyProProSerAlaMetThrPro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1801 ATTGTACAACAGGTGAAGCAGCAGGAGCAGAAA 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              556 IleLeuThrGlnValLysGlnHisGlnGlnGln 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC CONFATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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US-08-021-608D-2
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695 116 755 815 155

Db 475 rogly-ProglyThrProMetGlyPro 483  Qy 1938 AACGCAGCCAGATCGGAGCAAACCAAAGACCATCTGAGGAATGAGAAGTCTGCGG 1997  1938 AACGCAGCCAGATCGGAGCAAACCAAAGACCATCTGAGGAATGAGAAGTCTGCGG 1997  Db 484 TyrAsnProAlaProTyrAsnProGlyPro	QY 2055 GAAGGTCAGCCAGAACCACCGAGCCCCGCC 2093	GENERAL INFORMATION:  APPLICANT: LEVENS, DAVID L., DUNCAN,  APPLICANT: LEVENS, DAVID L., DUNCAN,  TITLE OF INVENTION: NOVEL FUSE BINDING  TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR  NUMBER OF SEQUENCES: 24  CORRESPONDENCES: 28  APPLICANT OF SEQUENCES: 24  APPLICANT OF SEQUENCES:	45 PARK P YORK W YORK USA DABLE FORE	COMPATING SYSTEM: PC-DOS/MS-DOS COFFRATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: FILING DATE: 04-OCT-1996 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: 04-OCT-1096 CLASSIFICATION NUMBER: 04-OCT-1096 NATION NUMBER: 04-OCT-1096	FILING DATE: 22-FEB-1993 CLASSIFICATION: 435 ATCRNEY/AGENT INFORMATION: NAME: WILLIAM S. FEILER REGISTRATION NUMBER: 26,728 REGISTRATION NUMBER: 26,728 TELECOMMUNIC/DOCKET UNMER: 2026-4063US1 TELECOMMUNIC/DOCKET UNMER: 2026-4063US1 TELEPHONE: (212) 758-4800	- 22 4 02 1 33 · 52 1	; CELL LINE: HL60 ; FEATURE: ; OTHER INFORMATION: ; OTHER INFORMATION: Amino Acid 149 (Xaa) is Met or Ile US-08-726-160-2 Alignment Scores: Fred. No.: 6.42e-13 Length: 644 Score: 245.00 Matches: 145 Fercent Similarity: 35.64\$ Conservative: 82 Best Local Similarity: 22.76\$ Mismatches: 169 Query Match: 169
	GCCAA LysGl GTGCT ::::: Leuil		STGGGCGC        ValGly11 SCCTCTAT	CAAGATTGCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCC	1537	OY 1593 GAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCTGGCCGGGTGATTGGCAAAGG 1652  Db 383	1762 435 1818 455 455

755 136 815 861

695

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1152 TCTGATCCCAGGGTTGAACCTCAGCGCACTTGGCATCTTTTCAACAGGACTGTCCGTGCT 1211
                                                                                                                                                                                                                                                                                             eProAlaSerLysAlaGlyLeuValIleGlyLysGlyGlyGluThrIleLysGlnLeuGl 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               972 ACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAACCC 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1032 GGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCCAGTGCTGAGATAGAGAT 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----LysProLeuArg-----IleThrGlyAspProTyrLysValGlnGlnAlaLysGl 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SerArgileGlyGlyAsnGluGlyIleAspValProlieProArgPheAlaValGlyIl 289
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eGlnPheLysProAspAspGly---ThrThrProGluArglleAlaGlnIleThrGlyPr 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oProAspArgCysGlnHisAlaAlaGluIleIleThrAspLeuLeuArgSerValGlnAl 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 aGlyAsnProGlyGlyProGlyProGlyGlyArgGlyArgGlyArgGlyGlnGlyAsnTr 368
                            aProGlnAsnAspSerPheGlyThrGlnLeu-----ProProMetHisGlnGlnGlnSe
                                                                                       :||| :::
97 rArgSerVal---MetThrGluGluTyrLysValProAspGlyMetValdlyPheileil
                                                               CGGAAAGGAGGCTTGACCATAAAGAACATCACTAAGCAGACCCAGTCCCGGGTAGATAT
                                                                                                                                                                                                                               ---GAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 CCCTCCTCACCTGCAGTGGGAGGTGTTGGATGGACTTTTGGCTCAATATGGGACAGTGGA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 GAATGTGGAACAAGTCAACACAGACACAGAAACGGCGGTTGTCAACGTCACATATGCAAC 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyGlyGly-GlyValAsnAspAlaPheLysAspAlaLeuGlnArg-----AlaAr 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gGlnIleAlaAlaLysIleGlyGlyAspAlaGlyThrSerLeuAsnSerAsnAspTyrGl 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GlyGlyĠly 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION: Amino Acid 149 (Xaa) is Met or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        644
145
82
241
169
27
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION
FILING DATE: 22-FEB-1994
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/021,608
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-4063PCT
TELEPROMOMICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPRAX: (212) 758-4800
TELEPRAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644
THENDER AMINO ACID
 ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01782
FILING DATE: 22-FEB-1994
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                                                                                                                                                                                                                                                                                      2026-4063PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Peptide/Protein HYPOTHETICAL: No
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245.00
35.64%
22.76%
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IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                        Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUB TYPE:
CELL TYPE:
CELL LINE: HL60
ORGANILLE:
FRATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Unknown
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
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336 CCCTCCTCACCTGCAGTGGGAGGTGTTGGATGGACTTTTTGGCTCAATATGGGACAGTGGA 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 gGlnIleAlaAlaLysileGlyGlyAspAlaGlyThrSerLeuAsnSerAsnAspTyrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 CCAGCGTGGGGACCACTCTTCCCGGGAGCAAGGCCACGCCCCTGGGGGGCACTTCTCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 oGlyPheHisHisGlyAspGlyProGlyAsnAlaValGln------GluIleMetIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516 CTICAAGATTICCIACATCCCGGATGAAGAGGTGAGCTCCCCTTCGCCCCCTCAGCGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 yTyrGlyGlyGlnLysArgProLeuĠluAspGlyAspGlnProAspAlaLysLysValAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 aProGlnAsnAspSerPheGlyThrGln-----LeuProProMetHisGlnGlnGl
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96 nArgSerVal---MetThrGluGluTyrLysValProAspGlyMetValGlyPhellell
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                                                                                                                                                                                                                                                                                                                                                                                    Amino Acid 148 (Xaa) is Met or Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643
145
81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ProSerSerGlySerAlaGlyGlyGlyGly
                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.72e-13
243.50
35.48%
22.76%
                                                                                                                                                      TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                   CELL LINE: HL60
FEATURE:
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Query Match:
                                                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                        643
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                                                                                                                                                                                                                                                                                                                                                                                                              US-08-021-608D-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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                                                                                           GAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCTGGCCGGGTGATTGGCAAAGG
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                                                                                                                       1653 TGGCAAGACCGTGAACGAACTGCAGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGA
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                            US-08-021-608D-10

Sequence 10. Application US/08021608D

Patent No. 5580760

GENERAL INFORMATION:

APPLICANT: LEVENSA, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: ROUTE FUSE BINDING

TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: 22-FEB-1993
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NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
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COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
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1762 ----TTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAACAGGTGAA 1817
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434 nIleAspTyrAlaArgGlnLeuIleGluGluLySIleGlyGlyProValAsnProLeuGl
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                 1392 CATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTAT
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                                                                                           CAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCC
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| OProAspArgCysGlnHisAlaAlaGluIleIleThrAspLeuLeuArgSerValGlnAl
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288 eVallleGlyArgAsnGlyGluMetIleLySLySIleGlnAsnAspAlaGlyValArgIl
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APPLICANT: AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF
APPLICANT: HEALTH AND HUMAN SERVICES
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
                                                                                                                                                                                                                                               ------GGACGGATCTTTGGGAAA-
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511 AsnAlaTyrProHisTrpGlnGlnGlnAlaProProAspProAla
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ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
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                                                                                                                                          59 yTyrGlyGlyGlnLysArgProLeudiuAspGlyAspGlnProAspAlaLysLysValAl 79
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115 eGlyArgGlyGlyGluGlnIleSerArgIleGlnGluSerGlyCysLysIleGlnIl
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                                                               eArgAspGlnGlydlyPheArgGluVal---
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; ZIP: 10154 ; COMPUTER READABLE FORM:	Db 79 aProGlnAsnAepSerPheGlyThrGlnLeuProProMetHisGlnGlnGl
ME N	ATTTCCCGCTGCGGATCCTGGTCCC
ORDPERF	:::                      Db 96 nArgSerValMetThrGluGluTyrLysValProAspGlyMetValGlyPhe1le1l
	696 CGGAAAGGAGG
ION DATA:	Db 115 eGlyArgGlyGluGlnileSerArgIleGlnGluSerGlyCysLysIleGlnil
; APPLICATION NUMBER: U.S. 08/021,608 ; FILING DATE: 22-FEB-1993	Qy 756 CCATAGAAAAGAGAACTCTGGAGCAAGCAAGCCTGTCACCATCCAT
INFORMATI AM S. FEIL	Db 135 eAlaProAspSerGlyGlyLeuProGluArgSerCys***LeuThrGlyThrProGl
; REGISTRATION NUMBER: 26,728 ; REFERENCE/DOCKET NUMBER: 2026-4063PCT	Qy 816 GGGGACTTCTGAAGCATGCGCGCATCTTGAAATCATGCAGAAA
(212) 758-4800	Db 154 uSerValGlnSerAlaLysArgLeuLeuAspGlnIleValGluLysGlyArgProAlaPr
12) 75 SEQ II	ттсстст
; SEQUENCE CHARACTERISTICS: ; LENGTH: 643	Db 174 oGlyPheHisHisGlyAspGlyProGlyAsnAlaValGlnGlulleMetIl
; TYPE: Amino Acid ; STRANDEDNESS: Single	Qy 912 ACACAAIGGCTIGGAGGACTGGITGGAAAAGAAGGAGGAGAAAITTGAAGAAAATTGA
螀	Db 191 eProAlaSerLysAlaGlyLeuVallleGlyLysGlyGlyGlyThrIleLysGlnLeuGl
Zμ	QY 972 ACATGAAACAGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAACCC
ORGANISM: Human	Db 211 nGluArgAlaGlyValLySMetValMetlleGlnAspGlyPr
INDIVIDUAL ISOLATE: DRVELOPMENTAL STACE.	atcactgtgaagggcacagttgaggcctgtg
]	:::        :::   Db 225 oglnAsnThr
CELL TYPE:	QY 1092 TATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGCTG
ORGANELLE:	Db 232LysProLeuArgIleThrGlyAspProTyrLysValGlnGlnAlaLysGl
NAME/KEY: LOCATION:	CAGGGTTGAACCTCAGCGCACTTGGCATCTTTCAACAGG
IDENTIFICATION METHOD:	Db 248 uMetVal
; OTHER INFORMATION: Amino Acid 148 (Xaa) is Met or 11e PCT-US94-01782-10	1212
Alignment Scores:	Db 254 eArgAspGlnGlyGlyPheArgGluVal
	Qy 1272 CCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCGTTCCCGCATCA
Conservative: Mismatches:	Db 264ArgAsnGluTyrGlyArgAsnGluTyrGly
3.98% Indels: 5 Gaps:	П
US-09-270-437D-6 (1-3412) x PCT-US94-01782-10 (1-643)	269
Oy 336 CCCTCCTCACCTGCAGTGGGGGTGTTGGATGGACTTTTGGCTCAATATGGGACAGTGGA 395	Т
Db 10 ProSerSerGlySerAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 22	288
QY 396 GAATGTGGAACAAGACAGAACAGAGAAACGGCGTTGTCAACGTCACATATGCAAC 455	QY 1452 CAAGATTGCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCC
· · · · AspAlaLeuGlnArg	805
456	OY 151Z ACCGGARAGCCCAGTICARGGCCCAG
Db 39 gGlnIleAlaAlaLysIleGlyGlyAspAlaGlyThrSerLeuAsnSerAsnAspTyrGl 59	
	Db 347 aGlyAsnProGlyGlyProGlyGlyArgGlyArgGlyArgGlyArgGlyArgGlyArgGlyArgTr
Ŋ	Qy 1555

TELEPHONE: (212) 758-4800  TELEPAX: (212) 751-6849  INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 590 TYPE: Antho Acid STRANDEDNESS: Single TOPOLOGY: Unknown MOLECULE TYPE: Peptide/Protein HYPOTHETICAL: No ORGINAL: SOURCE: ORGANISM: Human CELL LINE: HL60 -08-021-608D-8 ignment Scores: 3.48e-12	Qy         727 ACTAAGCAGACCCAGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAG 786           Db         111 GlnGlnGluSerGlyCysLysIleGlnIleAlaProAspSerGlyGlyLeuProGlu 129           Qy         787 AAGCCTGTCACCATCCATGCACCCCGAGAGGACTTCTGAAGCATGCAT	943 AAAGAGCAGAAATTTGAAGAAATTGAACATGAAACAGGACCAGATTAACAATTCAAGAAATTGAAGAAATTGAAGAAAATTGAAGAAAATTGAAGAA
Db   367 pAsnMetGlyProProGlyGlyLeuGlnGluPheAsnPhelle	1998 AGGGGCGAGGATCTGCCGAGGAGACCCCAGGGGCCGAGGGGCGGGG 2   1998 AGGCGGCCGAGGACTCTGCCGAGGGAGGGCCGAGGAGGGCCGAGGAGGGCCGAGGAG	

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1483 AGCGAAAGGATGGTCATCATCACCGGGCCACCGGAA---GCCCCAGTTCAAGGCCCCAG--- 1536
                                                                                                                                               --GGA 1539
                                                                                                                                                                                          1540 CGGATCTTTGGGAAA-----CTGAAAGAG 1563
                                                                                                                                                                                                                                                                                                                                         1684 ACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTG--- 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGATCAGGGAAATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTC 1848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2026 GAGAACCCCAGGGGCCGAGGAGGGGGGAAGGTCAGCCAGGTTTGCCAGAA----C 2079
1363 CTCTTCATCCCAACCCAGGCTGTGGGCGCCATCATCGGGAAGAAGGGGGGCACACATCAAA 1422
                                             1423 CAGCTGGCGAGATTCGCCGGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTC 1482
                                                                                                                                                                                                                                          1564 GAAAACTTCTTTAACCCCAAAGAAGAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCT 1623
                                                                                                                                                                                                                                                                                         1741 ATCGTCAGAATTATCGGGCAC------TTCTTTGCTAGCCAGACTGCACAGCGC 1788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1969 AGACCATCTGAGGAATGAGAAGTCTGCGGAGGCGGCCAGGGACTCTGCCGAGG---CCCCT 2025
               303 ProGluArglleAlaGlnIleThrGlyProProAspArgCysGlnHisAlaAlaGluIle 322
                                                                                                                                                                  323 IleThrAspLeuLeuArgSerValGlnAlaGlyAsnProGlyGlyProGlyFroGlyGly 342
                                                                                                                                                                                                            390 SerGlyAlaArglleGluLeuGlnArgAsnProProProAsnAlaAspProAsnMetLys 409
                                                                                                                                                                                                                                                                                                                                                                                                         430 LysIleGlyGlyProValAsnProLeuGlyProProValProHisGlyProHisGlyVal 449
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Sequence:

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Sequence 40, Appl
Sequence 500, Appl
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     Sequence 1116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-01-764-864-1116

Sequence 1116, Application US/09764864

Fatent No. US20020132753A1

GENERAL INFORMATION:

TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PT23

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1792

SEQ ID NO 1116

LENGTH: 620
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                  TYPE: PRT
ORGANISM: Homo sapiens

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6707.276 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Jatabase

Result

Qy         973 CATGAAACAGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAACCCG 1032           Db         323 HisGluThrGlyThrLyslleThrIleSerSerLeuGlnAspLeuSerIleTyrAshFro 342           Qy         1033 GAAAGAACCATCATGAAGGCACAGTTGAGGCTGTGCTGAGTTGATGAGATT 1092           Db         343 GluArgThrIleThrValLysGlyThrValGluAlaCysAlaSerAlaGluIleGluIle 362           Qy         1093 ATGAAGAAGCTGCTGAGGCTTTGAAATGATGATGCTGGCTG	Db   383	Qy         1333 CACTCTTATCCAGAGCAGAGATTGTGAATCCTTCATCCCCAACCCAGGCTGTGGGCGC 1392           Db         443 HisSerTyrProGludlnGlulleValAsnLeuPhelleProThrGlnAlaValGlyAla 462           Qy         1393 ATCATCGGGAAGAGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATC 1452           Db         463 IlelleGlyLysLysGJAAlaHisIleLysGlnLeuAlaAGJYAlaSerIle 482           Qy         1453 AAGATTGCCCCTGCCGGAAAGGCCCCAAACGTCAGCATCATCATCACCGGGCCA 1512	Db 483 LysileAlaProAlaGluGlyProAspValSerGluArgMetValileIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1633 GGCCGGGTGATTGGCAAAGGTGGCAAGCCGAACTGCAGACTTAACCAGTGCA	Qy         1753 ATCGGGCACTTCTTGCTAGCCAGACTGCACAGGGCAAGATGTACAACAG 1812	RESULT 2 US-10-313-986-501 Sequence 501, Application US/10313986 Publication No. US20030236209A1 GENERAL INFORMATION: APPLICANT: Foy, Teresa M. APPLICANT: MoNabb, Andria APPLICANT: Reed, Steven G. APPLICANT: Mang, Tongtong TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER FILE REFERENCE: 210121.455C19
Pred. No.:  Score:  Score:  Score:  Score:  3065.50  Matches:  Best Local Similarity:  97.73\$  Conservative:  Mismatches:  1  Query Match:  90.08\$  Indels:  3  Gaps:  US-09-270-437D-6 (1-3412) x US-09-764-864-1116 (1-620)  Qy  22 CGCCGGGTACCGGGCGGGGGCCGCGGGAAGAGGGCCGATG 72		3GAGC 31       	113 Leualadiniyedarkatususususususususususususususususususus	163 GlyHisGlnPheGluAsnTyrSerPheLysTieSerTyrTieProAspGluGluValSer 182	ACCCAGTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGGACATCACTAAG 73	4-5 5-5 F-0

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AAGATTGCCCCTGCGGAAGGCCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGGCCA 1512
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US-10-097-340-147
; Sequence 147, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: JOHN MONAHAN
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CURRENT APPLICATION NUMBER: US/10/313,
CURRENT FILING DATE: 2002-12-04
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SOFTWARE: FastSEQ for Windows Version
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Indels:
                                                                                             Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
Rosemarie SCHMANDT
       Sebastian HOERSCH
Shubbangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
Ami SEN
Manjula GANNAVARAPU
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SerArgLys1leGln1leArgAsn1leProProHisLeuGlnTrpGluValLeuAspGly	1030   CCGGAAAGAACCATCACTGTGAAGGCCAGTTGAGGCCTGTGCCAGTGCTGGGATAGAG   1089   1081
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118 IleLysIleAlaProAlaGluGlyProAspValSerGluAr 1510 CCACCGGAAGCCCAGTTCAAGGCCCAGCGACCGACCTTTTGG 438 ProProGluAlaGlnPheLysAlaGlnGlyArgIlePheGl 1570 TTCTTTAACCCCAAAGAAGAAGACGGAAGACGCATAT 458 PhePheAsnProLysGluGluValLysLeuGluAlaHisIl 1630 GCTGGCCCGGGTGATTGCCAAAGACGTGCAAGACGACAAAA 498 AlaGluValIleGlyLysGlyGlyGlyLysThrValAsnGl 1660 GCAGAACTCATCGTGCCACACACGCCAAAGACGCCAAA 498 AlaGluValIleGlyLysGlyGlyGlyGlyGlyArhrValAsnGl 1750 ATTATCGGGCACTTCTTTGCTAGCCAAACGCCCAAAGCGCAAA 498 AlaGluValIleValProArgAspGlnThrProAspGluAs 1750 ATTATCGGGCACTTCTTTGCTAGCCACACGCCAAAGCGCCAAA 498 AlaGluValIleValProArgAspGlnThrProAspGluAs 1750 ATTATCGGGCACTTCTTTGCTAGCCACACGCCAAAGCGCCAAA 498 AlaGluValIleValProArgAspGlnThrAlaGlnArgly 1810 CAGGTGAAGCACCAGAAATACCCTCAGGGAGCCCAAA 518 IleIleGlyHisPhePheAlaSerGlnThrAlaGlnArgly 1810 CAGGTGAAGCACCAGAAATACCCTCAGGGAGCCCAAA 518 IleIleGlyHisPhePheAlaSerGlnThrAlaGlnArgly 1810 CAGGTGAAGCACCAGAAATACCCTCAGGGAGCCCAAA 518 IleIleGlyHisPhePheAlaSerGlnThrAlaGlnArgly 1810 CAGGTGAAGCACCAGAAATACCTCAGGAGACCC 1810 CAGGTGAAGCACCAGAAATACCTCAGGAGACCCAAA 518 IleIleGlyHisPhePheAlaSerGlnThrAlaGlnArgly 1810 CAGGTGAAGCACCAGAAATACCCTCAGGGAGCCCAAA 518 IleIleGlyHisPhePheAlaSerGlnThrAlaGlnArgly 1810 CAGGTGAACTCAGGAGACCCAGAAATACCTCAGGAGACCAAA 518 IleIleGlyHisPhePheAlaSerGlnThrAlaGlnArgly 1810 CAGGTGAAGCAGAAATACCCTCAGGAGACCAAA 518 IleIleGlyHisPhePheAlaSerGlnThrAlaGlnArgly 1810 CAGGTGAAGCAGAAATACCCTCAGGAGACCAAA 518 IleIleGlyHisPheAlaSerGlnGlyValAla 518 IleIleGlyHisPheAlaSerGlnGlyValAla 518 IleIleGlyHisPheAlaSerGlnGlyValAla 518 IleIleGlyHisPheAlaSerGlnGlyValAla 518 IleIleGlyHisPheAlaSerGlnGlyValAla 518 ILECATACATON NUMBER: US/10/648,593 6URRENT APPLICATION NUMBER: OS/10/648,593 6URRENT PEPRICATION NUMBER: OS/10/648,593 6URRENT PEPRICATION NUMBER: OS/10/648,593 6URRENT PEPRICATION NUMBER: OS/10/648,593 6URRENT PEPRICATION NUMBER: OS/10/648,593 6URRENT PEPRICATION NUMBER: OS/10/648,593 6URRENT PEPRICATION NUMBER: OS/10/648,593 6URRENT PEPRICATION NUMBER: OS/10/648,593 6URRENT PEPRICATION NUMBER: OS/10/648,593 6URRENT PEPRICATION NUMBER: OS/10/648	Score

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PRIOR APPLICATION NUMBER: 60/329,414
PRIOR FILING DATE: 2001-10-15
PRIOR PLING DATE: 2001-10-17
PRIOR PLING DATE: 2001-10-17
PRIOR PLING DATE: 2001-10-17
PRIOR PLING DATE: 2001-10-22
PRIOR PLING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 60/343,629
PRIOR PLING DATE: 2001-10-24
PRIOR PLING DATE: 2001-10-24
PRIOR PLING DATE: 2001-10-29
REMAINING PAIC APPLICATION NUMBER: 60/349,575
PRIOR PLING DATE: 2001-10-29
ROMBER OF SEQ ID NOS: 133
SOFTWARE: CuraSeqList version 0.1
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Matches:
Conservative:
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CRCANISM: Homo sapiens
US-10-262-445-40
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Best Local Similarity:
Query Match:
DB:
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LENGIH: 555
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FILE REPERBENCE: 2146-24620
CURRENT APPLICATION NUMBER: US/10/262,445
CURRENT FILING DATE: 2002-10-01
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
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                                                                  1450 ATCAAGATTGCCCCTGCGGAAGGCCCCAGACGTCAAGGATGGTCATCATCACCGGG 1509
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                       398 AlaileileGlyLysLysGlyAlaHisileLysGlnLeuAlaArqPheAlaGlyAlaSer
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Ooi, Chean Eng
Patturajan, Mera
Rieger, Daniel
Spytek, Kimberly
Taupier Jr., Raymond J.
Zerhusen, Bryan
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Publication No. US0040014058A1
ADPLICANT ALSObrook II, John
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Chant, John
Chaudhuri, Amitabha
Edinger, Shlomit
Gerlach, Valerie
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Gorman, Linda
Guo, Xiaojia
Kekuda, Ramesh
Mezes, Peter
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Zhong, Mei
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   APPLICANT: MCNab, Andria
APPLICANT: MCNabb, Andria
APPLICANT: MCNabb, Andria
APPLICANT: Mcnabb, Andria
APPLICANT: Meach, Steven G.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
TENCEL CO. 2002
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Matches:
Conservative:
Mismatches:
Indels:
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                                                   Sequence 500, Application US/10313986
Publication No. US20030236209A1
GENERAL INFORMATION:
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2025.50
78.94%
65.67%
33.09%
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Best Local Similarity:
Query Match:
DB:
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US-10-313-986-500
                               RESULT 6
US-10-313-986-500
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Pred. No.:
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                                    CCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTTGAA
                                                ATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTTGAAAATCTTG
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                                   535 ValileValLysileIleGlyHisPheTyrAlaSerGlnMetAlaGlnArgLysIleArg
                                                                           APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REPERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/873,637
NUMBER OF SEQ ID NOS: 201-06-04
SOFTWARE: Patentin Ver. 2.0
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Matches:
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Patent No. US20020061543A1
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                  CCCTCTTCCACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACGTGAACGAGCCGTGAACGGAACTGCAG
                               CICITIGGGGACAGGAAGCIGCCCCIGGGGACAGGICCIGCIGAAGICCGGCIACGCC
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APPLICANT: POY, TETESA M.
APPLICANT: MCNabb, Andria
APPLICANT: Metanabe, Yoshihiro
APPLICANT: Reed, Steven G.
APPLICANT: Rend, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT APPLICATION NUMBER: 2002-12-04
NUMBER OF SEQ ID NOS: 560
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Conservative:
Mismatches:
Indels:
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LENGTH: 589
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Pred. No.:
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Chaitenya S.
APPLICANT: Bangur, Chaitenya S.
APPLICANT: Honser, Nancy
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Mang, Aljun
APPLICANT: Menderson, Robert A.
APPLICANT: Moneill, Patricia D.
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FILLE FERRENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US/09/735,705
CURRENT PILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Panger, Neil
TYTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERBNOS: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
EBMCTH: 579
TYPE: PRT
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                             Sequence 449, Application US/09897778

Patent No. US20020147143A1

GENERAL INFORMATION:
APPLICANT: Marnerakis, Margarita
APPLICANT: Marnerakis, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Garter, Darrick
APPLICANT: Garter, Darrick
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
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APPLICANT: APPLICANTON: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/697,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFWWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity:
Query Match:
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US-09-897-778-449
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SerValGlyAlaIleIleGlyLySGlnGlyGlnHisIleLysGlnLeuSerArgPheAla
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APPLICANT: Kalos, Michael D.
APPLICANT: Retex, Marc W.
APPLICANT: Retex, Neil
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APPLICANT: Peckman, David W.
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QQ	360 LeuGlnAlaHisLeuIleProGlyLeuAsnLeuAs	AlaLeuGlyLeuPhe 376
ΟΥ	1201 CIGTCCGTGCTATCTCCACCAGGGCCCCGGGAGCTCCCCCGGTGCCCCTACCAC	SCTCCCCCCCCCCTACCAC 1260
qq	377BroProThrSerGl	 MetProProThr 386
λŏ	1261 CCCTTCACTACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCG	TACCCCCATCACCAGTTTGGCCCG 1320
Dβ	387SerGlyProProSerAlaMe	ThrPro
٥٨	1321 ITCCCGCATCATCACTCTTATCCAGAGCAGAGATTGTGAAATCTTTCATCCCAACCCAG	GTGAATCTCTTCATCCCAACCCAG 1380
QQ	397 TyrProGlnPheGluGlnSerGluThrGluTh	
λŏ	1381 GCTGTGGGCGCCATCATCGGGAAGAAGGGGGCACACATCAACAGCTGGCGAGATTCGCC	ATCAAACAGCTGGCGAGATTCGCC 1440
Ωp	416 SerValGlyAlaileileGlyLysGlnGlyGlnHi	IleLysGinLeuSerArgPheAla 435
٥'n	1441 GGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGACGTCAGCGAAAGGATGGTCATC	GACGICAGCGAAGGAIGGICAIC 1500
qq	436 GlyAlaSerIleLysIleAlaProAlaGluAlaPr	AspalaLysValArgMetVallle 455
à	1501 ATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGATCTTTGGGAAACTGAAA	GGACGGATCTTTGGGAAACTGAAA 1560
qq	456 ileThrGlyProProGluAlaGlnPheLysAlaGl	GlyArgileTyrGlyLysileLys 475
λõ	1561 GAGGAAACTICTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATAICAGAGTGCCC	CTGGAAGCGCATATCAGAGTGCCC 1620
qa	476 GluGluAsnPheValSerProLysGluGluValLy	LeuglualaHisileArgValPro 495
ζλ	1621 TCTTCCACAGCTGGCTGATTGGCAAAGGTGGCAAGACCGTGAACGAAACC	AAGACCGTGAACGAACTGCAGAAC 1680
qq	496 SerPheAlaAlaGlyArgValIleGlyLysGlyGl	LysThrValAsnGluLeuGlnAsn 515
ζ	1681 ITAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTG	ACGCCAGATGAAATGAGGAAGTG 1740
qq	516 LeuSerSerAlaGluValValValProArgAspGl	Thr Prodepgludendendel
δ	1741 AICGICAGAAITAICGGGCACTICITIGCIAGCCAGACIGCACAGGGCAAGAICAGGGAAA	ACTGCACGCAAGATCAGGGAA 1800
Db	536 ValValLys1leThrGlyHisPheTyrAlaCysGl	ValAlaGlnArgLysileGlnGlu 555
ζŏ	1801 ATTGTACAACAGGTGAAGCAGCAGGAGCAGAAA 1	1833
qq	556 ileLeuThrGlnValLysGlnHisGlnGlnGln 56	9
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 Abul6583
Abu85652
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Abu16581
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23-AUG-2000; 2000US-00649167.
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WPI; 2001-639362/73.
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N-PSDB; AAS70981
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ABG06794;
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Abd06795 Human nov
Abg96794 Human nov
Aau16166 Human nov
Abu55235 Human sec
Aau16164 Human sec
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Result No.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal ectivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anno acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the vive of the sequences. Claim 20; SEQ ID NO 37153; 103pp; English. biodiversity  ${\tt H} \times {\tt W} \times {\tt SOSS} \times {\tt S$ 

Sequence 614 AA;

GTGTTGGATGGACTTTTGGCTCAATATGGGACAGTGGAAATGTGGAACAAGTCAACACA 417 58 GGGAAGAGGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCGCGCGTCACCGCC 117 AAGTCCGGCTACGCCTTCGTGGACTACCCCGACAGAACTGGGCCATCCGCGCCATCGAG AAAAAGCTAAGGAGCAGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAG GACACAGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAAGAAGAAAAAATAGCC ATGGAGAAGCTAAGCGGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCG GATGAAGAGGTGAGCTCCCCTTCGCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCC GACGACCTCCGGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTG ACCCTCTCGGGGTAAAGTGGAATTGCATGGGAAATCATGGAAGTTGATTACTCAGTCTCT 614 603 0 0 Conservative: Mismatches: Indels: Length: Matches: US-09-270-437D-6 (1-3412) x ABG06794 (1-614) 603.00 100.00% 100.00% 53.84% Percent Similarity: Best Local Similarity: Alignment Scores: 12 118 32 178 52 238 298 92 358 112 418 132 478 152 172 Query Match: DB: .. No Вb g g d g à g ⋧ 엄 ð à à à à à q δλ

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                                                       Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
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New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 11; SEQ ID NO 1116; 980pp; English

concoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a complete a medical condition or susceptibility to a lateral pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunosasays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune consenses e.g. rheumatoid arthritis, hyperproliferative disorders e.g. creptorascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. corneal infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before corpuspatiative, as a food additive or preservative to increase or decrease storage corpuspatities, as a food additive or preservative to increase or decrease storage corpuspatibites, fat content, lipid, protein, camponents. The present components components content in the specification of the present components and other nutritional components. The present components and other nutritional components. The present components and other nutritional components. The present components and other nutritional components. The present components and other nutritional components. The present components and other nutritional components. The present components and other nutritional components. The present components of the printed sequence data for this patent did not form part of the printed sequence. The invention relates to isolated nucleic acid molecules and their

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CCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCCAGTGCTGAGATAGAG
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New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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RUBEN S M.
BARASH S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-147444/14.
N-PSDB; ABX73491.
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                                                                                                                                                    14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                 14-AUG-2000;
14-AUG-2000;
22-AUG-2000;
30-AUG-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                              01-SEP-2000; 201-SEP-2000; 201
                                         26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-2000;
25-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
03-OCT-2000;
03-OCT-2000;
03-OCT-2000;
01-NOV-2000;
01-NOV-2000;
01-NOV-2000;
                                                                                                          14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                               05-SEP-2000;
05-SEP-2000;
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08-DEC-2000;
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The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, ployps and sinusitis, and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood

	OY 1030 CCGGAAAGAACCATCACTGAAGGGCACAGTTGAGGCTGTGCCAGGGTGAGATGAGAGGTGAGAGAGGTGAGAGAGGTGAGAGAGGTGAGAGAGGTGAGAGAGGTGAGAGAGGTGAGAGAGAGGTGAGAGAGGTGAGAGAGGTGAGAGAGGTGAGAGAGAGGTGAGAGAGAGAGAGGTGA	Qy 1150 AATCTGATCCCGGGGTTGAACCTCGGCATCTTTTCAACAGGACTGTCCGTG 1209	402 LeuSerProProAlaGlyProArgGlyAlaProProAlaAlaProTyrHisProPheThr 1270 ACCCACTCCGGATACTTCTCCCGCGTTACACCCCATCACCAGTTTGGCCCGTTCCCGCAT	422 IIITISSELDIYTTEREGISELIGUIYTTEREGISESTERIYATORI 1330 CATCACTCTATCCAGACAGAGAATTGTGAATTGTCATCCCAACCCAGGCTGTGGGC   1330 CATCACTCTATATCCAGGCTGTGGGC   142	1390	1450 AICAGARAIGCCCIGGGGGGGGGGGGGGGGGGGGGGGGGG	ProproglualaglnPheLysalaglnGlyArgllePheGlyLysLeuLysGluGluAsn TTCTTTAACCCCAAAGAAGAAGAAGGTGAAGGTGAAA 1602	522 PhePheAsnProLysGluGluValLysLeuGlusum. 4	AB AB	XX DT 13-FEB-2002 (first entry) XX XX DE Novel human diagnostic protein #6786.	Human; chromosome mappi food supplement; medica	OS Homo sapiens. XX XX PN W0200175067-A2.	FD 11-OCT-2001. XX PF 30-MAR-2001; 2001WO-US008631.	PR 31-MAR-2000; 2000US-00649167. PR 23-AUG-2000; 2000US-00649167. XX	PA (HYSE-) HYSEQ INC. XX
ed disorders (e.g. thrombosis, atheroscleros ction) and cancerous diseases. Sequences ABU 748 represent human novel polypeptides of th nce 620 AA; Scores:	0. No.: 51.00 cent Similarity: 100.00% ry Local Similarity: 100.00% ry Match: 45.62%	US-09-270-437D-6 (1-3412) x ABU55232 (1-620)  Qy 70 ATGATGAACAAGCTTTACATCGGAACCTGACCCCGCCGTCACCGCCGACGACCTCCGG 129	Qy 130 CAGCTCTTTGGGGACAGGAAGCTGCCCTGGCGGGACAGGTCCTGAAGTCCGGCTAC 189	Db   62 AlaPheValAspTyrProAspGlnAsnTrpAlaIleArgAlaIleGluThrLeuSerGly 81   Qy	310 AGCARARATTCABATTCABACATCCTCCTCCTCCTCGCGGGGGGGTTGGATGGA CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	Oy 370 CTTTTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACACAGACACACAGAAACC 429 Db 122 LeuLeuAlaGlnTyrGlyThrValGluAsnValGluGlnValAsnThrAspThrGluThr 141	OY 430 GCCGTTGTCAACGTCACATATGCAACAAGAAGAAGCAAAAATAGCCATGGAGAAGCTA 489 	Qy         490 AGCGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCGGATGAAGGTG 549           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 550 AGCTCCCCTTCGCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCCCGGGAGCAAGGC 609	Oy 610 CACGCCCTGGGGGCACTTCTCAGGCCACACAGATTGATTCCCGCTGCGCATCCTGGTC 669	OY 670 CCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACCATCACT 729	QY 730 AAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAG 789 	Qy         790 CCTGTCACCATCCATCCACCCCAGAGGGGACTTCTGAAACATGCCGCATGATTCTTGAA 849           Db         262 ProvalThrIleHisAlaThrProGluGlyThrSerGluAlaCysArgMetIleLeuGlu 281	850	11emetolinysolualanspolutininysbeuriasilalitistioseanyssiloida GCACACARATGGCTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAATT

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal crivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in company of mutations in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at the electronic format directly from WIPO at the cequences.
                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 37154; 103pp; English.
     Tang YT;
       Liu C,
                                                2001-639362/73
                                                                          N-PSDB; AAS70982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 594 AA;
Drmanac RT,
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CGGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTC 126 CGGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTGAAGTCCGGC 186 GGTAAAGTGGAATTGCATGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTA 306 AGGAGCAGGAAAATTCAGATTCGAAACATCCCTCCTCCTGCAGTGGGAGGTGTTGGAT 366 GGAGGAGGAGGAGGAGGCCGGGTACCGGGCCGGGGAGCCGCGGGCTCTCGGGGAAGAGA 66 187 TACGCCTTCGTGGACTACCCCGACAGAACTGGGCCATCGCGCCATCGAGACCCTCCG 594 378 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-09-270-437D-6 (1-3412) x ABG06795 (1-594) 378.00 100.00% 100.00% 33.75% Percent Similarity: Best Local Similarity: 18 29 38 127 247 307 Query Match: DB: à g à qq δλ a ð du à g à g ò

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<b>2</b> 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	427 A       158 T	ACCGCCGTTGTCAACGTCACATATGCAACAAGAAGAAGAAGAAAAAATAGCCATGGAGAAG 486
λ	7	AGAG 54
qq	78	renelysileSerTyrileProAspGluGlu 19.
\$ A	547 G     198 V	GTGAGCTCCCCTTCGCCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCCCGGGAGCAA 606
δ	607 G	99
QQ	218 9	m
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QQ	238 V	
8 8	727 A(	rn
3 6	) t	niinigineeneenigvalaspilenisargbyseluasnserelyalaalaglu 27
g g	78	Angecistateateateateetateetata 846 
ò	847 G	GAAATCATGCAGAAAAGAGGCAGATGAGCCCAAACTTAGCCGAAGAGATTCCTCTGAAAATC 906
qq	298 G	
δλ	0.2	TIGGCACACAATGGCTIGGTAGGAAGACTGATIGGAAAAAGAAGGAGAAATTTGAAGAAA 966
op O	318 Le	suAlaHisAsnGlyLeuValGlyArgLeulleGlyLysGluGlyArgAsnLeuLysLys 337
& A	967 A1 	TTGBACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATAC 1026
δλ	1027 A	CGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCCAGTGCTGAGATA 10
OP	358 As	, ,
δ	^	TATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGCTG
qq	œ	95
RESU ABG9 ID XX AC	5 6 696346 696346	andard, protein; 556 AA
X L	-DEC	(first entry
X E X	벌	an cancer marker M452.
KW CC KW CC KW Dr KW Dr KW Db	FENGERS	intral nervous system disorder; familial history; brain disorder; tral nervous system disorder; bacterial meningitis; viral meningitis; helmer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; in herniation; inflammation; encephalitis; testicular disorder; tuberculous granulomatous orchitis; connective tissue disorder; rt disorder; ischaemic heart disease; atherosclerosis; neoplasm; tological type; carcinoqenic; ovarian cancer marker.
X S X	₽	·n
NA X	20027192	-A2.
£8¥	19-SEP-2002	

Kovatis SG; , Mills GB;

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Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
                                                                                                                Monahan JE, Gannavarapu M, Hoersch S, Kamatkar S, Ko
Meyers RE, Morrisey MP, Olandt PJ, Sen A, Vieby PO,
Bast RC, Lu K, Schmandt RE, Zhao X, Glatt K;
                                                                                                                                                                                                                                       Disclosure; Page 263-264; 481pp; English
               14-MAR-2001; 2001US-0276025P.
14-MAR-2001; 2001US-0276026P.
10-AUG-2001; 2001US-0311732P.
19-SEP-2001; 2001US-0323580P.
26-SEP-2001; 2001US-0324567P.
26-SEP-2001; 2001US-0325102P.
                                                                             26-SEP-2001; 2001US-0325149P.
                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                   from a non cancer patient
                                                                                                                                                        WPI; 2002-723277/78.
N-PSDB; ABS76442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 556 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nvention
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The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the expression of the marker in a control non-ovarian cancer sample, where consideration. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as cossible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing cancer. The cancer markers may be used in the management and treatment cancer. The cancer markers may be used in the management and treatment of e.g. brain and central nervous system disorders (e.g. bacterial and viral meningitis, Alzaheimer's disease or Parkinson's disease), brain chilammations (e.g. bacterial or viral meningitis or brain herniations), inflammations (e.g. bacterial or viral meningitis or encephalitis), connective tissue disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with experient cancer mantering the progression of ovarian cancer, determining cancer or at risk of developing ovarian cancer. The present amino acid cancer represents one of the ovarian cancer markers described in the invention

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CAGCTCTTTGGGGACAGGAAGCTGCCCTGGCGGGACAGGTCCTGAAGTCCGGCTAC 189
                                                                                                                                               70 AIGAIGAACAAGCITIACAICGGGAACCIGAGCCCCGCCGTCACGCCGACGACCACCGGG
                                                                                                         556
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                           Conservative:
                                     Mismatches:
Indels:
        Length:
Matches:
                                                                            US-09-270-437D-6 (1-3412) x ABG96346 (1-556)
                357.00
100.00%
100.00%
31.87%
                                     Similarity:
                            Percent Similarity:
Alignment Scores:
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secreted protein, Seq ID 1119.

Human novel

1089 1029 300 729 220 789 849 260 606 280 696 320 200 249 369 100 429 120 489 549 160 609 180 699 9 80 ProvalThrileHisAlaThrProGluGlyThrSerGluAlaCysArgMetIleLeuGlu CCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAGATAGAG ATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTG GCACACAATGGCTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAAATT GAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAAC AAGCAGACCCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAG CCTGTCACCATCCATGCCACCCCAGGGGGACTTCTGAAGCATGCCGCATGATTCTTGAA CCCACCCAGTITGITGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACT GCCTTCGTGGACTACCCCGACCAGAACTGGGCCATCGCGCCATCGAGACCCTCTCGGGT AAAGTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAAGG CTTTTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAAGTCAACACAGACACAGAAACC GCCGTTGTCAACGTCACATATGCAACAAGAAGAAGAAGCAAAAATAGCCATGGAAGAAA AGCGGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTG AGCITCCCCITCGCCCCCCCAGCGAGCCCAGCGTGGGGACCACTCTTCCCGGGAGCAAGGC AAU16166 standard; protein; 171 790 241 850 1030 1090 301 341 201 730 221 AAU16166 181 061 250 310 81 370 101 430 121 490 141 550 61 AAU16166
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DE Hume 임 d dd à 음 ਨੇ d qq d à à ð ద ò g à d ð 셤 ð g ò ò g d à g ð δ ð

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Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide, opthalmalogical; vulnerary; secreted protein; rhematoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cardiovascular ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; conneal infection; ocular disorder; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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                                                                                                                                                                                                                                                                                                                                                               31-JAN-2000; 24-FEB-2000; 24-FEB-2000; 26-FEB-2000; 26-FEB-2000; 26-FEB-2000; 26-FEB-2000; 26-FEB-2000; 26-FEB-2000; 26-FEB-2000; 28-JUN-2000; 28-JUN-2000; 28-JUN-2000; 20-JUN-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JUL-2000; 26-JU
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ABU55235 standard; protein; 171 AA
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14-AUG-2000; 2
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14-AUG-2000; 2
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26-JUL-2000;
26-JUL-2000;
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22-AUG-2000;
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14-AUG-2000;
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28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals. cofactors and other nutritional components. The present sequence represents a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31
                                                                                                                                                                                                                                                                                                             New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and
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Matches:
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                                                                                                                                                                                                                                                                                                                                                    used as food additives or preservatives.
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               06-DEC-2000; 2000US-0251479P.

08-DEC-2000; 2000US-0251868P.

08-DEC-2000; 2000US-0251869P.

08-DEC-2000; 2000US-0251869P.

08-DEC-2000; 2000US-0251989P.

08-DEC-2000; 2000US-0251990P.
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2000US-0256719P
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                                                                                                                                GlnGlnValLysGlnGlnGlnGlnLysTyrProGlnGlyValAlaSerGlnArgSerLys 171
                                                                                                                                                                                                                                                      Human; neural disorder; immune system disorder; renal disorder; muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic;
AGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTC
                                                   1747 AGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTA
                                                                                         CAACAGGTGAAGCAGCAGCAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAAG
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2000US-0234274P.
2000US-0234997P.
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New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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                                                                                                                                                                                                                                                                               Barash SC;
27-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0236327P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236368P.
20-CT-2000; 2000US-0236802P.
02-CT-2000; 2000US-0236802P.
02-CT-2000; 2000US-023703PP.
02-CT-2000; 2000US-023703PP.
02-CT-2000; 2000US-023703PP.
03-CT-2000; 2000US-023703PP.
03-CT-2000; 2000US-023703PP.
03-CT-2000; 2000US-023409EP.
01-NOV-2000; 2000US-024188PP.
01-NOV-2000; 2000US-024188PP.
01-NOV-2000; 2000US-024180PP.
01-NOV-2000; 2000US-024180PP.
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2000US-0251868P.
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                                                                                                                                                                                                                                                                              Ruben SM,
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                                                                                                                                                                                                                                (ROSE/) ROSEN C A.
(RUBE/) RUBEN S M.
(BARA/) BARASH S C.
                                                                                                                                                                                                                                                                                                             N-PSDB; ABX73494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 171 AA;
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08-DEC-2000; 2
08-DEC-2000; 2
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The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. consentials, nearal polyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, c.g. congenital heart defects, Ebstein's anomaly and hypoplastic left chart syndromel, renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and spendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial cinfarction) and cancerous diseases. Sequences ABUS5494 and Myocardial conference ABUS5498 represent human novel polypeptides of the invention 171 160 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: 1e-142 160.00 100.00% 100.00% 14.29% Similarity:

US-09-270-437D-6 (1-3412) x ABU55235 (1-171) Percent Similarity: Alignment Scores: Best Local S. Query Match:

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1806 AACTICITIAACCCCAAAGAAGAGGIGAAGCIGGAAGCGCATATCAGAGIGCCCTCTICC 1626 1687 AGIGCAGAAGICAICGIGCCICGIGACCAAACGCCAGAIGAAAAIGAGGAAGIGAICGIC 1746 CAACAGGTGAAGCAGCAGAAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAAG 1866 GGGCCACCGGAAGCCCAGTTCAAGGCCCCAGGACGGATCTTTGGGAAACTGAAAGAGGAA 1566 SerAlaGluVall1eValProArgAspGlnThrProAspGluAsnGluGluVall1eVal 131 ThralaglyargvallleglybysglyglysThrvalAsngluLeuglnAsnLeuThr 111 The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were by prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can included. 5' ESTs are derived from mRNAs with intact 5' ends and can are also used to obtain full length cDNAs and genomic DNAs. 5' ESTs mapping proceedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors 16 71 Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping. AsnPhePheAsnProLysGluCluValLysLeuGluAlaHisIleArgValProSerSer 1747 AGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACGCGCAAGATCAGGGAAATTGTA diagnostic, forensic, gene therapy and chromosome mapping procedures. correspond to 5'ESTs and for New nucleic acid that is a 5' expressed sequence tag (5' EST) for Claim 13; SEQ ID NO 7342; 71pp + Sequence Listing; English. ٠<u>,</u> Giordano Human secreted protein, SEQ ID NO: 7342. CDNAs and genomic DNAs that Duclert A, Ā AAG03261 standard; protein; 97 21-FEB-2000; 2000EP-00200610. 99US-0122487P (first entry) Dumas Milne Edwards J, 2000-500381/45. WPI; 2000-500381/ N-PSDB; AAC03267. (GEST ) GENSET. Homo sapiens. 26-FEB-1999; EP1033401-A2 06-OCT-2000 06-SEP-2000. 1567 obtaining 22 72 92 112 132 1807 152 AAG03261; AAG0326 RESULT 9 q 셤 g à 셤 à ò 셤 장 ð

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2000US-0217496F

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       Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer; a disease; infection; ocular disorder; council proliferation; schaeming; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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04-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0184664P.
16-MAR-2000; 2000US-0189350P.
16-MAR-2000; 2000US-0189374P.
19-MAY-2000; 2000US-0199123P.
19-MAY-2000; 2000US-0198123P.
19-MAY-2000; 2000US-0209467P.
28-JUN-2000; 2000US-0214886P.
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Barash SC, Ruben SM; Rosen CA,

WPI; 2001-488783/53. N-PSDB; AAS26151 New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 11; SEQ ID NO 1117; 980pp; English

prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition to susceptibility to a pathological condition to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays invention relates to isolated nucleic acid molecules and their

04-FEB-2000; 2000US-0180628P. 28-JUN-2000; 2000US-0214886P. 07-JUL-2000; 2000US-0216647P.

17-JAN-2001; 2001US-00764864. 31-JAN-2000; 2000US-0179065P.

US2002132753-A1.

19-SEP-2002

Homo sapiens.

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diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. creoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. cerebral ischaemia, angiogenesis, carevous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, cornespantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemocaxis. The polypeptides can also be used cornerate tissues and in chemocaxis. The polypeptides can also be used corpainties, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present capabilities, fat some nutritional components. The present corpused for this patent did not form part of the printed
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New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular orenal disorders.
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14-A0G-2000; 2000US-0225268P.
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14-A0G-2000; 2000US-0225268P.
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08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                      11-JUL-2000; 2
14-JUL-2000; 2
26-JUL-2000; 2
26-JUL-2000; 2
14-AUG-2000; 2
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The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinusitis), reproductive disorders, east rounders disorders, congenital heart defects, pulmonary disorders, ardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and

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1113
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                                                                                                                                                                                                                                                        994 ACAATCTCATCTTTGCAGGATTTGAGCATATACAACCGGAAAGAACCATCACTGTGAAG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide, opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiac arthritis; hyperproliferative disorder; cerebral isohaemia; angiogenesis; nervous system disorder; Alzheimer; disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                             131
                                                                                                                                                                                                                                                                                                                           92 GlyrhrvalGluAlaCysAlaSerAlaGluIleGluIleMetLysLysLeuArgGluAla 111
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leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                     1054 GGCACAGITGAGGCCTGTGCCAGTGCTGAGATAAGAGAAGAAGCTGCGTGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                         1174 AGCGCACTTGGCATCTTTCAACAGGACTGTCCGTGCTATCTCCA 1218
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Gaps:
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6.70%
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Best Local Similarity:
                                                                                         Sequence 192 AA;
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28-JUN-2000;
30-JUN-2000;
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24-FEB-2000;
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2001US-0259678P
20-OCT-2000;
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01-NOV-2000;
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06-DEC-2000;
08-DEC-2000;
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01-DEC-2000;
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(HUMA-) HUMAN GENOME SCI

CA, Barash SC, Rosen

WPI; 2001-488783/53 N-PSDB; AAS26570.

and New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions diagnosing, preventing, treating or amelused as food additives or preservatives.

Claim 11; SEQ ID NO 1536; 980pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic

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immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays

(ELISA). Disorders which are diagnosed or treated include autoimmune
diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.

cliseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.

carest, cerebrovascular disorders e.g. cerebral isohaemia, angiogenesis,

carest, cerebrovascular disorders e.g. cerebral isohaemia, angiogenesis,

carest, verbrovascular disorders e.g. Alzheimer's disease, infections caused by

carest, viruses and fungi and ocular disorders e.g. corneal infection,

and many other disorders listed in the specification. The polypeptides

can also be used to aid wound healing and epithelial cell proliferation,

con also be used to aid wound healing and epithelial cell proliferation,

con prevent skin aging due to sunburn, to maintain organs before

cremerate tissues and in chemotaxis. The polypeptides can also be used

cregenerate tissues and in chemotaxis. The polypeptides can also be used

credentitities, fat content, lipid, protein, carbohydrate, vitamins,

capabilities, fat content, lipid, protein, carbohydrate, vitamins,

credeneral cofactors and other nutritional components. The present

sequence represents a novel secreted protein of the invention. Note: The

sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1609 ATCAGAGTGCCCTCTTCCACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAAC 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1669 GAACTGCAGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAA 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1729 AATGAGGAAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGC
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66
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Matches:
Conservative:
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04-FEB-2000; 2000US-0180628P.
28-JUN-2000; 2000US-0214886P.
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The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders; immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal vestibulitis, nasal polyps and sinustis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage
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RUBEN S M.
BARASH S C.
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Taupier RJ,
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                                                                                                                                                                                                   (e.g. Hodgkin's disease and
renal disease), hyperproliferative disorders (e.g. Hodgkin's disease a leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial inflarction) and cancerous diseases. Sequences ABUS4914-ABUS5699 and ABUS5748 represent human novel polypeptides of the invention
                                                                                                                                                                                                                            GAACTGCAGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAA
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                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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09-OCT-2001; 2001US-0327917P.
09-OCT-2001; 2001US-0328029P.
12-OCT-2001; 2001US-0328449P.
15-OCT-2001; 2001US-0329414P.
17-OCT-2001; 2001US-0339144P.
17-OCT-2001; 2001US-033142P.
22-OCT-2001; 2001US-0341058P.
23-OCT-2001; 2001US-034162P.
24-OCT-2001; 2001US-0344957P.
25-UNOV-2001; 2001US-0346557P.
25-UNOV-2001; 2001US-0346557P.
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66.00
100.00%
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5.89%
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                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                     Sequence 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                       Alignment Scores:
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DAPK3 polypeptide, useful for preparing a composition for treating or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125
                                                                                                                                                                                The invention describes an isolated polypeptide comprising any of 33 90-1273 amino acid sequences (I) given in the specification or its mature form, a sequence that is at least 95 % identical to (I), or a sequence comprising one or more conservative substitutions in the amino acid sequence of (I). The polypeptide is useful for preparing a composition for treating or preventing e.g. cancer. This is the amino acid sequence of a novel human NOV protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anorectic, antiinflammatory, cardiant, hypotensive, antidiabetic, neuroprotective, pharmaceutical composition, body-weight regulation, thermogeneais, metabolic, obesity, Syndrome X, insulin-resistance, eating disorder, cachexia, diabetes mellitus, hypertension, gallstone, pancreatic dysfunction, arteriosclerosis, coronary heart disease, hypercholesterolaemia, dyslipidaemia, osteoarthritis, ROS defence, reactive oxygen species, neurodegenerative, mitochondrial, gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGACAGTGGAGAATGTGGAACAAGTCAACACAGACACAGAAACCGCCGTTGTCAACGTC
     Spytek KA;
     Rieger DK,
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Matches:
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Mismatches:
 Patturajan M,
ng H, Zhong M;
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CE, Pattura
Zhong H,
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human; IGF-II mRNA binding protein 3
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                                                                                                                                                 Claim 2; Page 129; 253pp; English.
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2002EP-00003473.
2002EP-00004687.
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44.00
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                                                                                                                   preventing e.g., cancer.
   llet I,
Zerhusen
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                                                 2003-381704/36.
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Best Local Similarity:
                                                WPI; 2003-381704/
N-PSDB; ACA90176.
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14-FEB-2002; 2
28-FEB-2002; 3
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2000US-0226868F

2000US-0227182P

2000US-022924P

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 Homo sapiens.
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1510 CCACCGGAAGCCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAAAC 1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide, opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; antisopenesis; nervous system disorder; Alzheimer; disease; infection; ocular disorder; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
                                                                                                                                                                                                                                             The invention relates to a novel pharmaceutical composition comprising a nucleic acid molecule or polypeptide which is a human homologue of a Drosophila melanogaster polypeptide or polymucleotide. The composition of the invention may be utilised during the diagnosis, study, prevention of treatment of diseases related to body-weight regulation and thermogenesis including metabolic disorders such as obesity, Syndrome X and insulinesistance syndrome and eating disorders e.g. cachexia, diabetes mellitus, hypertension, pancreatic dysfunctions, arteriosclerosis, osteoarthritis and galistomes. Furthermore, disorders related to reactive oxygen species (RoS) defence may be addressed by the invention including neurodegenerative disorders or mitochondrial disorders. Finally, the composition of the invention may be useful in gene therapy. The current sequence is that of the human IGF-II mRNA binding protein 3 protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New pharmaceutical composition, useful for the manufacture of an agent for diagnosing, treating or preventing disorders related to body-weight regulation and thermogenesis, e.g., metabolic diseases such as obesity.
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Mismatches:
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Matches:
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                                                                                                                                                                                                                         Claim 3; Fig 7C; 144pp; English.
 25-APR-2002; 2002EP-00009475.
18-JUN-2002; 2002EP-00013329.
30-DEC-2002; 2002EP-00029081.
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01-DEC-2000; 200005-0250160P.

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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in calleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune (Stasasse e.g. tremmatoid arthritis, hyperproliferative disorders e.g. crebrovascular disorders e.g. crebral isorders e.g. crebral isorders e.g. crebral isorders e.g. arrest, cerbral disorders e.g. disorders e.g. corneal infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to capenerate tissues and in chemotaxis. The polypeptides can also be used crapabilities, fat content, lipid, protein, cambohydrate, vitamins, capabilities, fat content, lipid, protein, cambohydrate, vitamins, minerals, cofactors and other nutritional components. The present compensate or the printed sequence data for this patent did not form part of the printed
                                                                                                                                                   New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.
                                                                                                                                                                                                                                                             Claim 11; SEQ ID NO 1534; 980pp; English.
                           Ruben SM;
                                                                     WPI; 2001-488783/53.
N-PSDB; AAS26568.
                         Rosen CA,
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643 AFTGATTICCCGCTGCGGATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAG 702 US-09-270-437D-6 (1-3412) x AAU16581 (1-47) ð

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Conservative: Mismatches: Indels:

Length: Matches:

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Alignment Scores:

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RESULT 1
US-09-261-855-20

Sequence 20, Application US/09261855A

Patent No. 6255055

GENERAL INFORMATION:
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE

TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE

TURRENT APPLICATION NUMBER: US/09/261,855A

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.0

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Sequence 7570, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                      452 ArgMetVall1elleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArglle 470
                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6255055

GENERAL INFORMATION:
APPLICANT: ROSS, JEFÍTEY
TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (FAD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960.26(c,9.951.1)
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENT VET. VET. 2.0
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REPERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT PILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOCTHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
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Indels:
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Bangur, Chaitanya S.
Hosken, Nancy
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Li, Samuel X.
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Fan, Liqun
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                                                                                                                                                                                                   ORGANISM: Mus musculus US-09-261-855-2
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Best Local Similarity:
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Query Match:
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                                                                                                                                                       SEQ ID NO 2
LENGTH: 577
TYPE: PRT
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1489 AGGATGGTCATCATCACGGGCCACCGGAAGCCCCAGTTCAAGGCCCAAGGACGGATC 1545
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                                                                                                                                 APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hosken, Nancy
APPLICANT: Applicant: Gary R.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Menderson, Robert A.
APPLICANT: McMedil, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455511
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
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Sequence INCRAMATION

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Tongtong

APPLICANT: Hosken, Liqun

APPLICANT: Hosken, Nancy A.

APPLICANT: Ralos, Michael D.

APPLICANT: Ralos, Michael D.

APPLICANT: Ralos, Michael D.

APPLICANT: Ralos, Michael D.

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APPLICANT: Ralos, Michael D.

APPLICANT: Ralos, Michael D.

APPLICANT: Ralos, Michael D.

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C6

CURRENT APPLICATION NUMBER: US/09/480,884A

CURRENT FILING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 330

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 176

LENGTH: 579
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SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 348, Application US/09643597; Patent No. 6426072; GENERAL INFORMATION:
                                                                                                               Kalos, Michael D.
Bangur, Chaitanya S
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
Wang, Aijun
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
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ORGANISM: Homo sapiens
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US-09-480-884A-176
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Similarity: 100.00%
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US-09-606-421B-176
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Pred. No.:
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                                                   1489 AGGATGGTCATCATCACCGGGCCACCGGAAGCCCAGGTTCAAGGCCCCAGGGACGGATC 1545
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                                                                          452 ArgMetValllelleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArgIle 470
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APPLICANT: Ralos, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Panger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILLE REPERBENCE: 21012.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILLING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kalos, Michael D. APPLICANT: Ralos, Michael D. APPLICANT: Bangur, Chaitanya S. APPLICANT: Horken, Nancy A. APPLICANT: Horken, Nancy A. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REPERBACE: 210121455G8 CURRENT APPLICATION NUMBER: US/09/542,615A CURRENT FILING DATE: 2000-04-14 NUMBER OF SEQ ID NOS: 350
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Matches:
Conservative:
Mismatches:
Indels:
               US-09-270-437D-6 (1-3412) x US-09-480-884A-176 (1-579)
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FastSEQ for Windows Version 3.0
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FastSEQ for Windows Version 3.0
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; Sequence 176, Application US/09542615A
; Patent No. 6518256
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Patent No. 6518256
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Ligun
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ORGANISM: Homo sapiens
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Best Local Similarity:
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APPLICANT: Wang, T
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SEQ ID NO 176
LENGTH: 579
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LENGTH: 579
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APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE THERAPY
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APPLICANT: Wang, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER,
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT APPLICATION NORDER: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
                                                                                      US-09-270-437D-6 (1-3412) x US-09-542-615A-348 (1-579)
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CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF ESQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
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Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur. Chaitanya S.
APPLICANT: Hosken, Nancy
                                                                                                                                                                                                                                                                    Sequence 176, Application US/09606421B; Patent No. 6531315; APPLICANT: Wang, Tongtong APPLICANT: Pan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
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Query Match:
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US-09-270-437D-6 (1-3412) x US-09-261-855-21 (1-47)
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US-09-261-855-21
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                                                                                                                                                                                                                                                                                                                                 US-09-261-855-24

Sequence 24, Application US/09261855A

Sequence 24, Application US/09261855A

GENERAL NO. 6255055

GENERAL INFORMATION:

APPLICANT: Ross, Jeffrey

TITLE OF INVENTION: (TRD-BE) AND ITS NUCLEIC ACID SEQUENCE

FILE REFERENCE: 960296.95131

CURRENT PAPLICATION UNMERR: US/09/261,855A

CURRENT PLING DATE: 1999-03-03

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 24

LENGTH: 48
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| Sequence 22, Application US/09261855A
| Sequence 22, Application US/09261855A
| GENERAL INFORMATION:
| APPLICANT: Ross, Jeffrey
| TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
| TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
| TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
| CURRENT APPLICATION NUMBER: US/09/261,855A
| CURRENT HILING DATE: 1999-03-03
| NUMBER OF SEQ ID NOS: 46
| SEQ ID NO 22
| LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AlaGlyArgVallleGlyLysGlyGlyLysThrValAsnGluLeuGlnAsnLeu 25
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Matches:
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Mismatches:
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Mismatches:
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CORGANISM: Homo sapiens
US-09-261-855-24
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CORGANISM: Homo sapiens
US-09-261-855-22
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Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
 TYPE: PRT
CRGANISM: HOMO
US-09-606-421B-348
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Pred. No.:
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Sequence 21, Application US/09261855A
Fatent No. 625055
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: (RDD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REPERBNCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT ROSA, JEÉTERY
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (SRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (SRD-BP) AND ITS NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: (SRD-BP) AND ITS NUCLEIC ACID SEQUENCE
CURRENT APPLICATION NUMBER: 195/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 18
                                                                                                                                            925 GITGGAAGACTGATTGGAAAAGGCCAGAAATTTGAAGAAATTGGAA 972
                                                                                                                                                             925 GIIGGAAGACIGAIIGGAAAAGAAGGCAGAAAIIIGAAGAAA 966
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Sequence 23, Application US/09261855A
Patent No. 625605
GENERAL INFORMATION:
APPLICANT: Ross, Jeffrey
TITLE OF INVENTION: (TRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REPERENCE: 960296.95131
CURRENT APPLICATION UNBER: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Application US/09261855A
; Sequence 19, Application US/09261855A
; Patent No. 6255055
; General INFORMATION:
APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/261,855A
; CURRENT FILING DAIE: 1999-03-03
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
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; ORGANISM: Mus musculus
US-09-261-855-19
                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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Search completed: July 16, 2004, 11:30:45

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Sequence 501, App Sequence 1116, App Sequence 1119, App Sequence 119, App Sequence 1119, App Sequence 1119, App Sequence 1119, App Sequence 200, App1 Sequence 476, App Sequence 1132, App Sequence 1114, App Sequence 1114, App Sequence 1114, App Sequence 1116, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 1176, App Sequence 446, App Sequence 449, App Sequence 449, App Sequence 449, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Sequence 446, App Se
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APPLICANT: MoNabb, Andria
APPLICANT: Metanabb, Yoshihiro
APPLICANT: Red, Steven G.
APPLICANT: Red, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER;
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOOTHWARE: FRAELSEQ for Windows Version 4.0
US-09-764-864-1116
US-09-764-864-1116
US-09-764-864-1119
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US-09-773-20
US-10-313-986-476
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US-09-817-778-176
US-09-817-778-146
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US-10-113-986-446
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; Publication No. US20030236209A1
; GENERAL INFORMATION:
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    ORGANISM: Homo sapiens
    JS-10-313-986-501
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Len Mat Con Mis Ind Gap -313-986-	1 MetAsnlysLeuTyrIled	Qy         193 TTGGTGGATGAGGACTGGGGCCCTCTGGGGGATAA           LING	313 AGGAAAATTCAGAATCGAAACATCCCTCCTCACCTGCAGTGGGAGGTGTTGGATGGA	Db 101 LeuAlaGinTyrGlyThrValGludsnValGluGinValAsnThrAspfnrGlufnrAla 120 Qy 433 GTTGTCAACGTCACATATGCAACAAGAGAAGAAGAAAAATAGCCATGGAGAAAGCTAAGC 492 Db 121 ValValAsnValThrTyrAlaThrArgGluGluAlaLysIleAlaMetGluLysLeuSer 140 Qy 493 GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATGCCGGATGAAGAGGTGAGG	Db		Db 201 ThrGlnPheValGlyAlaileileGlyLysGluGlyLeuThrileLysAsnileThrLys 220 Qy 733 CAGACCCAGTCCCGGGTAGATATCCATAGAAAGAGAACTCTGGAGCTGCAGAGAAGCCT 792	OY 793 GTCACCATCCATGCCACCCCAGAGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATC 852 Db 241 ValThrileHisAlaThrProGludlyThrSerGluAlaCysArgMetileLeuGluile 260	nangaggcagargagaccaaacragccgaagagarrccrcrgaaaarcrrggca 91 	rrgaa 972        eGlu 300	Qy 973 CATGAAACAGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAACCCG 1032

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322 GluHisGluThrGlyThrLysIleThrIleSerSerLeuGlnAspLeuSerlleTyrAsn
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Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: JOHN MONAHAN
APPLICANT: Sebastian HOERSCH
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Steve G. KOVATS
Rachel B. MEYERS
Michael MORRISEY
Peter OLANDT
Ami SEN
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Gordon B. MILLS
Robert C. BAST, C
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Karen GLATT
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APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14 1510 CCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGGAAACTGAAAGAGGAAAAC 1569 501 521 ProProGluAlaGlnPheLysAlaGlnGlyArg1lePheGlyLySreuLysGluGluAsn TTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAA 1602

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PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR PRILING DATE: 2001-03-26
PRIOR PRILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR PRILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/24,967
PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001/09/26
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
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PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.05
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Sequence 182, Application US/10648593
| Publication No. US20040106132A1
| Publication No. US20040106132A1
| GENERAL INRORMATION:
| APPLICANT: Bristol-Myers Squibb Company
| TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THA
| TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
| TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
| FILE REPRENCE: DO273 NP
| CURRENT APPLICATION NUMBER: US/10/648,593
| CURRENT FILING DATE: 2003-08-26
| PRIOR PRIOR PRILING DATE: 2002-08-27
| NUMBER OF SEQ ID NOS: 557
| SOFTWARE: PATENTIN VERSION 3.2
| SEQ ID NO 182
| LENGTH: 556
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301 GluHisGluThrElyThrEysIleThrIleSerSerLeuGlnAspLeuSerIleTyrAsn
                                                                                           ATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTG
                                                                                                                                                                                                                                                                261 IleMetGlnLysGluAlaAspGluThrLysLeuAlaGluGluIleProLeuLysTleLeu
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1447 TCTATCAAGATTGCCCCTGCGGAAGGCCCCAGACGTCAGGGAAGGATGGTCATCATCAC
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ORGANISM: Homo sapiens
FEATURE:
LOCATION: (71)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
LOCATION: (147)
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1117
LENGTH: 192
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Matches:
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US-09-764-864-1117
Sequence 1117, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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        ; NUMBER OF SEQ ID ; SOFTWARE: Patentil; SEQ ID NO 1119 ; LENGTH: 171 ; TYPE: PRT ; TYPE: PRT | TYPE: PRT | TYPE: PRT | TYPE: PRT | TYPE: PRT | US-09-764-864-1119
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Pred. No.:
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                                        AlaPheValAspTyrProAspGlnAsnTrpAlalleArgAlalleGluThrLeuSerGly
                         AAAGTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAGG
                                                                        CTTTTGGCTCAATATGGGACAGTGGGAATGTGGAACAAGTCAACACAGAGACACAGAAACC
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Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICAMT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE PEPRENCE: P7223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
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US-09-764-864-1119
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TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS TITLE OF INVENTION: THE SAME
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PRIOR PILING DATE: 2001-10-05
PRIOR PILING DATE: 2001-10-05
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
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PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-09
PRIOR PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/328,414
PRIOR APPLICATION NUMBER: 60/329,414
PRIOR PILING DATE: 2001-10-15
PRIOR PILING DATE: 2001-10-25
PRIOR PILING DATE: 2001-10-22
PRIOR PILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/341,658
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
PRIOR PILING DATE: 2001-10-24
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                                                                                                                   GAACTGCAGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAA
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                                            US-09-270-437D-6 (1-3412) x US-09-764-864-1536 (1-171)
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CURRENT APPLICATION NUMBER: US/10/262,445
CURRENT FILING DATE: 2002-10-01
    Gaps:
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Taupier Jr., Raymond J.
Zerhusen, Bryan
Zhong, Haihong
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Sequence 40, Application US/10262445
Publication No. US20040014058A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John
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Chaudhuri, Amitabha
Edinger, Shlomit
Gerlach, Valerie
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Catterton, Elina
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Patturajan, Meera
Rieger, Daniel
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Kekuda, Ramesh
Mezes, Peter
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                                                        LOCATION: (160)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KRY: SITE
LOCATION: (164)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KRY: SITE
LOCATION: (165)
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         of the naturally occurring L-amino acids
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NAME/KEY: SITE
LOCATION: (55)
COCHER INFORMATION: Xaa equals any of the naturally occurring L-amino
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT223

FILE REFERENCE: PT223

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper NUMBER: OF SEQ ID NOS: 1792

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1536

LENGTH: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1174 AGCGCACTTGGCATCTTTCAACAGGACTGTCCGTGCTATCTCCA 1218
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
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Matches:
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              INFORMATION: Xaa equals any
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ORGANISM: Homo sapiens
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; OTHER INFORMATION:
US-09-764-864-1536
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Best Local Similarity:
Query Match:
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DB:
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LOCATION: (168)
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US-09-764-864-1536
                                    NAME/KEY: SITE
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TYPE: PRT
CORGANISM: Mus musculus
US-09-873-637-20
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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US-10-117-982-476
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Pred. No.:
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Pred. No.:
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US-09-873-637-20
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                                                                                                                                                                                                                                                                                               106 GlyThrValGluAsnValGluGlnValAsnThrAspThrGluThrAlaValValValAsnVal 125
                                                                                                                                                                                                                                                                            385 GGGACAGTGGAGAATGTGGAACAAGTCAACACAGACACAGAAACCGCCGTTGTCAACGTC 444
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APPLICANT: Monabb, Andria
APPLICANT: Metanabe, Yoshihiro
APPLICANT: Metanabe, Yoshihiro
APPLICANT: Metanabe, Yoshihiro
APPLICANT: Mananabe, Yoshihiro
APPLICANT: Mananay Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 499
HENGHH: 20
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APPLICANT: Rosen et al.
ITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 499, Application US/10313986; Publication No. US20030236209A1; GENERAL INFORMATION:
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 40
LENGTH: 555
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US-10-262-445-40
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US-10-313-986-499
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US-09-764-864-1534
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Pred. No.:
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; NAME/KEY: SITE
; LOCATION: (24)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1534
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Fatent No. US20020061543A1

GENERAL INFORMATION:

APPLICANT: Ross, Jeffrey

TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE

FITE REPERENCE: 960296.95131

CURRENT APPLICATION NUMBER: US/09/873,637

CURRENT FILING DATE: 2001-06-04

NUMBER OF SEQ ID NOS: 46

SEQ ID NO 20

LENGTH: 48
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1534
LENGTH: 47
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Mismatches:
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Matches:
Conservative:
Mismatches:
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Matches:
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; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Carter, Darrick; APPLICANT: Watanabe, Yoshihiro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 476, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
    APPLICANT: FORMATION:
    APPLICANT: McNabb, Andria
; APPLICANT: McNabb, Andria
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
; FILE REPERENCE: 210121.455C19
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTRARE FARISEQ for Windows Version 4.0
       APPLICANT: Mericle, Barbara

APPLICANT: Mericle, Barbara

APPLICANT: Mericle, Barbara

APPLICANT: Spies, Gregory A.

APPLICANT: Spies, Gregory A.

APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REPERRACE: 21012.455C18

CURRENT APPLICATION NUMBER: US/10/117,982

CURRENT PILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 484

SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
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Matches:
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Henderson, Robert A.
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ORGANISM: Homo sapiens
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US-10-117-982-476
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Best Local Similarity:
Query Match:
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US-09-764-864-1532
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US-10-313-986-476
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Pred. No.:
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LENGTH: 81
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 AlaGlyArgVallleGlyLysGlyGlyGlyLysThrValAsnGluLeuGlnAsnLeuThr 190
                                                                                                                            Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1332
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT223
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT APPLICATION NUMBER: US/09/764,864
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1114
LENGTH: 261
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFRENCE: PT223
CURRENT APPLICANT MUBBE: US/09/764,864
CURRENT FILING DATE: 2001-01-17
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Matches:
Conservative:
Mismatches:
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Mismatches:
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; ORGANISM: Homo sapiens
US-09-764-864-1114
                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
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us-09-270-437d-6.0ligo.rapb

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July 21, 2004, 06:04:06; Search time 12960 Seconds (without alignments)
11410.990 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Description	Seque Seque Isola Homo Seque Seque Seque Isola Homo	BX537583 Homo sapi AC016961 Homo sapi AC134942 Homo sapi AC126373 Homo sapi BD221443 Human gen AC126373 Homo sapi AC068379 Homo sapi AC126372 Homo sapi AC126372 Homo sapi AC126372 Homo sapi AC126372 Homo sapi AC126379 Homo sapi AC206404 Human gen AC209284 Sequence BD22C404 Human gen AX198757 Sequence	Sequence Sequence Sequence Sequence Sequence Sequence Secreted IAF-3591 IAF-3591 Mus mus Mus mus Mus mus Mus mus Sequence Secreted Secrete	AC026579 Homo sapi AP004290 Homo sapi AC104980 Homo sapi AX335143 Sequence linear PAT 17-DEC-2001 E., Jager, E., Alexander, K.
SUMMARIES	AR171865 AR34074 BD209925 BC021290 AR171867 AR343076 AR343076 AF117107 AF057352	HSN806243 AC116961 AC114942 AC126373 AC126373 AC126373 AC068379 AC068379 AC068379 AC068379 AC068379 AC068379 AC068379 AC068379 AC068379 AC068379 AC068379	,	COOSESTORMENTS PRODAZSO COLO4980 X335143 ALIGNMENTS 3412 bp DNA US 6297364. 5 Sang,S., Stockert,
Length DB	10 mm m m m m m m m m m m m m m m m m m	2640 998945 008243 008243 20820 22846 22846 364 364 364	4,000,0	.2259 2 .7226 9 .7226 9 .7301 9 .7226 9 .7300 6 .7317910 .103412) .103412) .103412)
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OS Homo sapiens (human)

PN 17 200512049-A/4

PD 23-APR-2002

PF 16-MAR-1999 UP 2000545030

PR 17-APR-1999 US 09/061709

PI ALEXANDER KNUTH, LLOYD J OLD

PC C12N15/09, A61K39/00, A61K39/39, A61P35/00, C07K16/32, PC

C12N1/15,

PC C12N1/21, C12N5/10, C12P21/08, C12Q1/68, G01N33/53, G01N33/ PC
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Organism='Homo sapiens (human)'.

Location/Qualifiers
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/organism="Homo sapiens"
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Patent: JP 2002512049-A 4 23-APR-2002;
LUDWIG INSTITUTE FOR CANCER RESEARCH
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3412 bp DNA linear PAT 17-JUL-2003
Isolated nucleic acid molecules encoding cancer-associated
antigens, these antigens and method of using the same.
BD209925.1 GI:33019695
JP 2002512049-A/4.
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: ALC.

CDNA Library Preparation: ALC.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing Dy: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Whe Site: http://www.nisc.nih.gov/

Contact: nisc mgc@nhgri.nih.gov/

Contact: nisc mgc@nhgri.nih.gov/

Rakher,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Blakesley,R.W., Cranite,S., Guan,X., Gupta,J., Haghighi,P.,

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McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,E.D.
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KILAHGLVGRLIGKEGRNLKKIBHETGTKTISSLQDLSIYNDFRITYUKGTVEACA
SABIBINKKLREAFENDWLANOQANLIPGLNLSALGIFSTGLSVLSPPAGFRGADPA
APYHPFTTHSGYFSSLYPHHQFGPPPHHHGYPEQETVNLFIFTGNAVALIGKGAALIK
QLARFAGASIKLARABGEDVSERWIITGPPEAQFKAQGRIFGKLKEENFFNPKEEVK
LEAHIRVPSSTAGRRIGKGGKTVNELQNLTGSAEVIVPRDQTPDENEEVIVRIIGHFFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.govSeries: IRAL Plates 39 Row: o Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27552765.
                                                                                                                                                                            Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                            URL: http://mgc.nci.nih.gov
this sequence version replaced gi:18204200.
                          human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="RRM; Region: RNA recognition motif"
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                                                                                                                                                                                                                                                                                                  VIH-MGC Project URL: http://m
On Aug 19, 2003 this sequence
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens IGF-II mRNA-binding protein 2, mRNA (cDNA clone MGC:29539 IMAGE:5090334), complete cds.
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QY         3125 GCGTTAAATTCACAGATTTTTTTAACGAGAAAACACACAGAAGAAGCTACCTCAGGTGT         3184           Db         3120 GCGTTAAATTCACAGATTTTTTTAACGAGAACACACACAGAAGATCCTCCTCAGGTGT         3179           QY         3185 TTTTACCTCAGACCTTGCTGTTTCCCTTAGAGATTTTGTAAAGCTGATAGTTGG         3244           Db         3180 TTTTACCTCAGCACCTTGCTGTTTCCCTTAGAGATTTTGTAAAGTTGG         3239           QY         3245 AGCATTTTTTTAATTAAAAAAAAAAAAAAAAAAAAAAAA	RESULT 5 AR171867 LOCUS DEFINITION Sequence 8 from patent US 6297364. AR171867 AR171	Design Match  Best Local Similarity 100.04; Pred. No.0;  Matches 2143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Matches 2143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Matches 2143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  1270 ACCCACTCCGGATACTTCTCCAGCCTGACCCCCATCACCCAGTTTGGCCGTTCCCGCAT 1220  Db 1141 ACCACTCCTATCCAGAGCAGATTTGTGAATCTCTTCATCCCAACCCGTTCGCGCT 1220  CV 1330 CATCACTCTTATCCAGAGCAGTTTGTGAATCTCTTCATCCCAACCCGGTTGGCCTT 1449  Db 1201 CATCACTCTTATCCAGAGCAGTTTGTGAATCTCTTCATCCCAACCCAGGCTTGGGC 1260  CV 1390 GCATCATCGGGAAGAAGGAGTTTGTGAATCTCTTCATCCCAACCCAGGCTTGGGC 1260  CV 1390 GCATCATCGGGAAGAAGGAGTTTGTGAATCTCTTCATCCCAACCCAGGCTTGGGC 1260  CV 1350 GCATCATCGGGAAGAAGGAGTTTGTGAATCTCCAACCAGGCTGTGGGC 1260  CV 1350 GCATCATCGGGAAGAAGGAGTTTGTGAATCTCCAACCAGGCTGTGGGC 1260  CV 1351 ATCAAGATTGCCCCTGCGGAAGGATTCGGCGAAATTCGCCGGAGCTCTT 1320  CV 1560 ATCAAGATTGCCCTGCGGAAGGCCCAACACGCTGAGGGAAACTTGAAAGAGGAAAAC 1569  Db 1321 ATCAAGATTGCCCTGCGGAAGGCCCAACGAACGCAAAGGATCCACCAGGCTTTTGGGAAAACTGAAAGAGGAAAAC 1569  Db 1381 CCACCGGAAGCCCAGTTCAAGGCCCAACGAACGCAAAACTTGAAAACTGAAAACAGGAAAAC 1569  Db 1381 CCACCGGAAAGCCCAAGGAAGCCCAAGGAAACTTTGGGAAAACTGAAAAGAGGAAAAC 1569  Db 1381 CCACCGGAAAGAAGAAGAAGAAGCTGGAAAACTGAAAGGAAAACTGAAAACAGAAAAACAGAAAAACAGAAAAACAGAAAAACAGAAAAACAGAAAAACAGAAAAACAGAAAAAA
2046 AGGGGCGGGAAAGGTCAGCCAGAACCACCGAGCCCCGCCTCCCGCCCCCA 2105 2041 AGGGGCGGGAAAGGTCAGCCAGTTTGCCAGAACCACCGAGCCCCGCCTCCCGCCCCCA 2105 2041 AGGGGCGGGGAAGGTCAGCCATTTGCCAGAACCACCCGAGCCCCCCCA 2100 2106 GGGCTTCTGCAGCGTTCAGCCATTCACCATCCATCGCTCCTCGAACTCCC 2165 2101 GGGCTTCTGCAGCGTTCAGCCATCCATTCACCATCCTCGAACTCCC 2160 2166 ACGACGCTATTCAGTCAACTAACATAAGATAACTTCAGAACTCCC 2160 2167 ACGACGCTATTCCTTTTAGTTCAACTAACATAACATAAGATAACTTCAAAGCCAACAAAT 2220 2226 GCACACCCTTTTTGTTGAAAATAACTAACATAAGAAAAT 2220 2226 GCACACCCTTTTTCTGTGCCAAATCGTTCTTTTGTAAAAATTTTAGAAAAGGAAA 2280 2236 GATGTTAAAAATATTTCTGTGGCAAATCGTCTTTTTTTTT	2346 AAATAATATATCAAATAACTCAATTTTTAATCAATTATTTTTT	2641 TIGCTICACAGGITTIAAACTGGITTITITICALIACIACTGCTATATAATTCTCTCTCTCC 2700 2706 TGTTTATCTCTCCCCTCCCCTCCCCTCTCTCTCTCTCTCT

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09   2770   CCCCCCANCTCANCCCCTANCCCCCCCCCCCCCCCCCCC	RESULT 6 RESULT 6 REASONA BA343076 LOCUS DEFINITION Sequence 8 from patent US 6576756. ACCESSION RA343076.1 GI:33738478 VERSION AR343076.1 GI:33738478 VERSION AR343076.1 GI:33738478 KEYWORDS SOURCE ORGANISM Unclassified. Unclassified. Chen, YT. (Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K. and Old, L., Green, YT. (Gure, A., Tsang, S., Stockert, E., Jager, E., Alexander, K. and Old, L., Green, CT. (Green, Reference) TITLE Isolated mucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof JOHNAL Patent: US 6576756-A 8 10-UUN-2003; FRATURES L. 3288 Location/Qualifiers Location/Qualifiers Source //mol_type="genomic DNA" ORIGIN Ouery Match Pest Local Similarity 100.0%; Pred. No. 0; Matches 2143; Conservative 0; Mismatches 0; Indels 0; Gaps O; Matches 2143; Conservative 0; Mismatches 0; Indels 0; Gaps O;
1501   GCTGGCCGGGTGATTGGCCAAACACCCAATGAAATGAGAACTTAACCAGT   1560     1690   GCAGAAGTCATCGTCCCCGGGCCAAACGCCAATGAAAATGAGGAAGTGATCGTCAA   1210     1561   GCAGAAGTCATCGTCCCCGTGACCCAACGCCAAATGATGATGATCGTCAAA   1620     1562   GCAGAAGTCATCGTTGCTCGCCAACGCCAAATGATGATGATGATCGTCAAA   1620     1563   GCAGAAGTCATCGTTGCTTGCACACCCCAACACCACACGCAAATTGTACAA   1680     1611   ATTATCGGGCACTTCTTTGCTAACCCCAACTCACACGCCAAGATCATCAAA   1680     1612   ATTATCGGGCACTTCTTTGCTAACACTCACACACCCTCAACGCGAAATTGTACAA   1680     1614   ATTATCGGGCACTTCTTTGCTAAATTACCCTCAAGGCCAAAATTGTACAA   1680     1616   ACGTCAACCACACACAAAATACCCTCAAGGCCAAGATCATCAAA   1680     1617   ATTATCGGGCACCACACAAAATACCCTCAAGGCCTCAACACCTCAACACTCAAA   1680     1618   CAGTCAAACCACACAAAAAAAAAAAACACCTCAAGGCACACCACACACA	2350 AATATATCAAATAACTCAACTAACTCCAATTTTTAATCAATTATT

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SQTAQRKIREIVQQVKQQEQKYPQGVASQRSK"
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                                                                                                                                                                                                 /gene="IMP-2"
/note="binds multiple sites in IGF-II mRNA
                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                               /product="IGF-II mRNA-binding protein
/protein_id="AAD09827.1"
/db_xref="GI:4191610"
                                                                                                                                        /note="alternative start-codon gives N-terminal methionine"
                    /mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens IGF-II mRNA-binding protein 2 (IMP-2) mRNA, complete
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Submitted (30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
Location/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Nielsen, J., Christiansen, J., Lykke-Andersen, J., Johnsen, A.H., Wewer, U.M. and Nielsen, F.C.
A family of insulin-like growth factor II mRNA-binding proteins represses translation in late development
Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
                    AAATTCACAGATTTTTTTAACGAGAAAAACACACAGAGAAGAAGCTACCTCAGGTGTTTTTA
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I (bases 1 to 3667)
Zhang, J.Y., Chan, E.K., Peng, X.X. and Tan, E.M.
A novel cytoplasmic protein with RNA-binding motifs is an autoantigen in human hepatocellular carcinoma
J. Exp. Med. 189 (7), 1101-1110 (1999)
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N. Torrey Pines Road, La
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Homo sapiens hepatocellular carcinoma autoantigen (p62)
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Zhang, J.Y., Chan, E.K.L., Peng, X.X. and Tan, E.M. Direct Submission
Submitted (03-APR-1998) Molecular & Experimenta Scripps Research Institute, 10550 N. Torrey Pin CA 92037, USA
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1994   CATAGGTGBACGTGTTCAAAGCCAAGCAAATGCACCCTTTTTCTGTGGCAAATGGTC   172	2794 CGCACCCCCCCCCCCCCCGGCAAAGCGGCTCTGAGTATCACATCACAAAAGGAACA 2072 2013 GGCACCCCCCCCCCCCCGGGCAAGCGGTGCTCTGGTTACACACAC
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Submission
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Homo sapiens 3 BAC RPI1-394J21 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
                              2493 GAGTTGGAAAAAAAAAAAATAAGATATCAACTGCCAGCCTGGAGAAAGGTGACAGTCCAAGTGTG 2552
GAGTTGGAAAAAAATAAGATATCAACTGCCAGCCTGGAGAAGGTGACAGTCCAAGTGTG 3332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                             3333 CAACAGCTGTTCTGAALTGTCTTCCGCTAGCCAAGAACC 3371
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Worley, K.C.
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Worley, K.C.
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standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plocal mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the BST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Housten, TX 77030, USA
GD Dec 28, 2002 this sequence version replaced gi:21908412.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
Submitted (21-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 98945)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
                                                                                                                                                                                                                                           Department
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                                                                                                                                                                                                                   Submitted (28-DEC-2002) Human Genome Sequencing Center, Departmer of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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585. .975
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    .98945
    organism="Homo sapiens"

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/db_xref="taxon:9606"
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50. .2004
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/rpt_family="AluY"
1762. .1834
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/rpt family="T-rich"

AUTHORS

repeat_region complement(1835, .2121) /rpt family="AluJo"	OV 1834 TACCITCAGGGAGTCGCCTCACAGGGAGGGAGGCTC	CACAGGACCAGGAAAAG 1893
repeat_region 21222133 /rpt familv="T-rich"		275
repeat_region complement(21362454)	1001	1 0
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repeat_region 2945repart_region 2946repart_region 2946repart_region 2946	# NO. 0	, ,
repeat_region		
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/rpc_ramily="Alusg" repeat_region 46144652		207
/rpt_ramily="A1_rich" repeat_region complement(49065202)	27474	274
/rpt_tamily="AluSx" repeat_region complement(52255526)		
/rpt_family="AluSp" repeat region 56645938	Db 27414 CAGAACCACGAGCCCGCCCCCCCCCCCAAGGGCTTCTG	akkichtekkenteken 27355
	Qy 2134 TCACCACTCGGATCTCTCTGGACTCCCACGCTATCCCTTTTAGTTGAACTAA	CCCTTTTAGTTGAACTAA 2193
	Db 27354 TCACCATCCACTCGGATCTCTCTGAACTCCCACGACGCTA	CCCTTTTAGTTGAACTAA 27295
	Qy 2194 CATAGGTGAACGTGTTCAAAGCCAAAATGCACCCT	Tricigiecaaarcerc 2253
repear_region comprement(/202/498) /rpt family="Aluy"	HILLINITOPA AGCCAAGCAAAATGCACACC	
repeat_region 85278569		
repeat_region 85798882		CCIGIGGGIIA
/rpt_family="AluSx" repeat region 8895. 9195	Db 27234 TCTGTACATGTGTGTACATATTAGAAAGGGAAGATGTTAAG	rardrectrereserra 27175
	Qy 2314 CACAGGGTGCCTGCAGCGGTAATATTTAGAAATAATAT	TCAAATAACTCAACTAAC 2373
repeat_region 9488951/ /rpt family="(TTTTG)n"	Db 27174 CACAGGGTGCTGCAGGGGTAATATATTTAGAATAATATATAATAATAATAATA	
repeat_region complement(95189798)	, p. c.	
repeat_region 1021-11-11-11-11-11-11-11-11-11-11-11-11-1		2433
/rpc_ramily="(1TA)n" repeat_region complement(1024110522)	DD 27114 TCCAATTTTTAATCAATTATTAATTTTTTTTTTTTTAAA	AGAAAGCAGGCITITITA 27055
/rpt_family="AluSx" repeat region complement(1059810893)	Qy 2434 GACTTTAAAGAATAAAGTCTTTGGGAGGTCTCACGGTGTAGAGAGGAGCTTTGAGG	GAGGAGCTTTGAGGCCAC 2493
	Db 27054 GACTTTAAAGAATAAAGTCTTTGGGAGGTCTCACGGTGTAG	caddadcriridaddccac 26995
	Qy 2494 CCGCACAAAATTCACCCAGAGGAAATCTCGTCGGAAGGAC	CTCACGGCAGTTCTGGAT 2553
	Db 26994 CCGCACAAATTCACCCAGAGGGAAATCTCGTCGGAAGGACACTCACGGCAGTTCTGGAT	CTCACGCCAGTICTGGAI 26935
	Ov 2554 CACCTTSTATISTABLE CACEGRATE CONTRACTOR CONTRACT	GGAAACTCTGTCACTCT 2613
STS 1299413178		
/standard_idame="tadogav4" misc_feature 13504, .13692	26934	
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	Db 26874 CATGCCTGTCTAGCTCATACACCCATTCTCTTTGCTTCAC	GGTTTTAAACTGGTTTTT 26815
	Qy 2674 TGCATACTGCTATATAATTCTCTGTCTCTCTGTTTATCT	TCCCCTCCCTCCC 2733
repeat_region complement(14314. 14622)	1000	
repeat_region complement(4625.14911)	# 1007 1007	07
/rpt_ramily="Alusp" repeat_region 1563815696	273	
/rpt_family="MER112" repeat_region 1569715716	Db 26754 CTTCTTCCATCTTTTTGAATTTCCTCATCCTTC	ArcrcaarcccGrarcra 26695
	Qy 2794 CGCACCCCCCCCCCAAAGCAAAGCAGTGCTCTGAGTATCACATCACAAAAAGGAACA	CATCACACAAAGGAACA 2853
Similarity 99.9%; Pred. No. 0; 3; Conservative 0; Mismatches 0;	Db 26694 CGCGCCCCCCCAGGCAAAGCAGTGCTCTGAGTATC	266
AGACTGCACAGGCAAGATCAGGGAAATTGTACAACAGGTGAAGCAGCAGGAGGAGCAGAAA 18	285	2913
Db 27714 CAGACTGCACAGCGCAAGATCAGGGAAATTGTACAACAGGTGAAGCAGGAGCAGAAA 27655	Db 26634 AAAGCGAAACACACAAACCAGCCTCAACTTACACTTGGTTA	TCAAAAGAACAAGAGTCA 26575

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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is
                  Oragunye,N., Oviedo,R., Pace,A., Payton,B., Perry,J., Perrez,L., Oragunye,N., Oviedo,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubkan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Stutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,R., Tang,H., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Walliams,G., Williams,G., Williams,G., Williams,G., Williams,G., Wolley,K., Washington,C., Walliamson,A., Wleczyk,R., Wooden,S., Worley,K., Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (03-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 208273)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conter clone name: RP11-164H23

------ Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 203806 bases at least Q40
Consensus quality: 207317 bases at least Q20
Consensus quality: 227337 bases at least Q20
Estimated insert size: 200535; sum-of-contigs estimation
Quality coverage: 10x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
Direct Submission
Submitted (27-MAR-2003) Human Genome Sequencing Center, Departmen Submitted (27-MAR-2003) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Mar 27, 2003 this sequence version replaced gi:27819431.
   Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G.,
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contig of 1362 bp in length
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks; S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbord, C., Burch, P., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Erown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burket, C., Burrell, K.L., Byrd, N.C., Chavez, D., Chavez, D., Char, S., Chen, Z., Chowdhry, I., Christopoulos, C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chavez, D., Davis, C., Davy-Carroll, I., Dedarich, D.A., Davis, C., Davy-Carroll, I., Dedarich, D.A., Delandy, K.R., Deladdo, O., Davy-Carroll, I., Dedarich, D.A., Delandy, K.J., Delandy, K.J., Delandy, C., Escotto, M., Falls, T., Ferraguto, D., Flaggar, D., Elwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaggar, N., Foster, P., Frantz, P., Garcia, A., Garner, T., Garza, N., Gill, R., Gao, J., Gavevara, W., Gunzerfine, P., Haves, A., Hanrandez, J., Harris, K., Harris, K., Harris, K., Harlak, P., Haves, A., Joudah, S., Rarlsson, E., Kelly, S., Rhue, J., Hulyk, S., Hune, J., Jud, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Luna, R., Massey, E., Manhiney, E., Martindal, J., Morsis, S., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mitchell, T., Mohabbat, K., Morgan, M., Nguyen, N., Newtson, J., Nguyen, N., Nguyen, N., Newtson, J., Nguyen, N., Nguyen, N., Nguyen, N., Newtson, J., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N.,
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26514 ACCAAACAAAGAAAAAATTCCACAATGAAAGAATGTATTTTGTCTTTTTGCATTTTTGGTG
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2314 CACAGGGGGCCTGCAGCGGTAATATTTTTGAAATAATATTCAAATAACTCAACTAAC 2373 81521 CACAGGGGGCCTGCAGCGGTAATATTTTTGAAATAATATATCCAAATACTCAACTAAC 81462 2374 TCCAATTTTTAATCAATTATTATTTTTTTTTTTTTTAAAGAAAG	2794 CGCACCCCCCCCCCCCGGGCAAAGCAGTGCTCTGAGTATCACATCACACAAAAGGAACA 2853 81041 CGCACCCCCCCCCCCCCGGGCAAAGCAGTGCTCTGAGTATCACACACA
8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6	8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6
## 11751   13080; contig of 1330 bp in length   ## 13081   13180; contig of 1350 bp in length   ## 13181   14705; contig of 1525 bp in length   ## 14706   14805; cap of unknown length   ## 14806   15952; cap of unknown length   ## 16533   17793; contig of 1749 bp in length   ## 17791   17890; gap of unknown length   ## 20675   20775; gap of unknown length   ## 20776   20775; cap of unknown length   ## 20776   20775; gap of unknown length   ## 20776   20775; gap of unknown length   ## 20776   20775; gap of unknown length   ## 20776   20775; gap of unknown length   ## 20776   20775; gap of unknown length   ## 20776   20775; gap of unknown length   ## 20776   20775; gap of unknown length   ## 20780   20790; gap of unknown length   ## 20780   20790; gap of unknown length   ## 20780   20100; gap of unknown length   ## 20790   20100; gap of unknown length   ## 20790   20100; gap of unknown length   ## 20790   20100; gap of unknown length   ## 20790   20100; gap of unknown length   ## 20790   20100; gap of unknown length   ## 2000   20100; gap of unknow	Query Match         38.0%; Score 1296; DB 2; Length 208273;           Best Local Similarity 9.8%; Pred. No. 0;         Andels 3; Gaps 2;           Best Local Similarity 9.8%; Pred. No. 0;         Andels 3; Gaps 2;           Watches 1556; Conservative 0; Mismatches 0; Indels 3; Gaps 2;         Andels 3; Gaps 2;           QY 1774 CAGACTGCACAGGCAAGATCACAGGACACAGGACAGACAG

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contig of 742 bp in length gap of 100 bp contig of 738 bp in length gap of 100 bp contig of 707 bp in length gap of 100 bp contig of 742 bp in length gap of 100 bp contig of 772 bp in length gap of 100 bp contig of 772 bp in length gap of 100 bp contig of 773 bp in length gap of 100 bp contig of 773 bp in length gap of 100 bp contig of 773 bp in length gap of 100 bp contig of 739 bp in length gap of 100 bp contig of 739 bp in length gap of 100 bp contig of 734 bp in length gap of 100 bp contig of 747 bp in length gap of 100 bp contig of 747 bp in length gap of 100 bp contig of 747 bp in length gap of 100 bp contig of 747 bp in length gap of 100 bp contig of 747 bp in length
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Chong, J., Chazaro, B., Chong, J., Chang, J., Chang, J., Chong, J., Chong, J., Chong, J., Chong, J., Chong, J., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardham, J., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K., Liu, G., Maclean, C., Maadonald, P., Major, J., Mathews, C., McCarthy, M., Meldrim, J., Moneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Merga, V., Punnkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rovery, P., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sanith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Leseasty, S., Theodore, B., Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:

Smit, A.F. A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/Repeatmasker.html
                                                HTG 05-JUL-2002
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 50320)
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                                ACL26373 50320 bp DNA linear HTG 05-JUJ
Homo sapiens chromosome 18 clone CTD-2307113 map 18, LOW-PASS
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
------------- Project Information
Center project name: 1.27661
Center clone name: 2307_1_13
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of 714 bp in length
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Homo sapiens chromosome 18, clone CTD-2307I13
Unpublished
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HTG; HTGS_PHASE0.
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1 (bases 1 to 710)
Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S., Reinhard, C., Giese, K., Randazzo, F., Kennedy, G.C., Pot, D., Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M., and Crain, B.S.
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  2625 AGCTCATACACCCATTTCTCTTTGCTTCACAGGTTTTAAACTGGTTTTTTGCATACTGCT
                                                                                             10520 AGCTCATACACCCCATTTCTCTTTTGCTTCACAGGTTTTTAAACTGGTTTTTTGCATACTGCT
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60/085696,21-OCT-1998 US 60/105234 PR
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larity 100.0%; Pred. No. 2.5e-309;
Conservative 0; Mismatches 0;
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/mol type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
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f 100 bp
f 760 bp in length
f 100 bp
g of 744 bp in length
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of 749 bp in length
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49446: contig of 750 bp in length
49546: gap of 100 bp
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
/map="18"
/clone="CTD-2307113"
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of 782 bp
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8: contig of 744 br
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FEATURES Source

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Aas58609 cDNA #128	Add71082 Human IGF	Aas58739 cDNA #141	Aav87489 EST clone	Ach18272 Human adu	Aah86031 Human sin	Aas57938 cDNA #614	Aca90176 cDNA enco	Aaa41968 Human sec	Aas58053 cDNA #729				Abl64217 Stomach c	Aas26568 Human cDN	Abx73909 Human nov	Aaa02581 Human col	Aal57525 Human IGF	Aai86673 Human pol	Ach39118 Human foe	Abq22104 Oligonucl	Abq22105 Oligonucl
AAS58609	ADD71082	AAS58739	AAV87489	ACH18272	AAH86031	AAS57938	ACA90176	AAA41968	AAS58053	ABV56560	ABL67315	ABN94637	ABL64217	AAS26568	ABX73909	AAA02581.	AAL57525	AA186673	ACH39118	ABQ22104	ABQ22105
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## ALIGNMENTS

Knuth A, Cancer associated antigen; KOC-3; cancer; vaccine; CT7; ss. Jager E, DNA encoding cancer associated antigen KOC-3. Stockert E, AAZ36152 standard; DNA; 3412 BP (LUDW-) LUDWIG INST CANCER RES. 98US-00061709. 99WO-US005766. Tsang S, (first entry) WPI; 2000-013284/01. Gure A, Homo sapiens WO9954738-A1. 16-MAR-1999; 17-APR-1998; 28-0CT-1999. 11-FEB-2000 AAZ36152; Chen Y, RESULT 1 AAZ36152 

old LJ;

Nucleotides representing cancer-associated genes, used to develop products for the diagnosis, monitoring and treatment of cancers.

Claim 55; Page 41; 44pp; English.

designated KCC-3. The specification also describes a cancer associated antigen designated CT7. The CT7 polynuclectide was isolated from SK-MEL-37 metalnom acells. The polypeptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAY43877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polynucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony present sequence represents a cancer associated antigen gene

ova

Human

AAS25126 AAS25356 AAH83772

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AAS24943 AAH83588

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AAS58000

Aas58000

ova ova ova CDNA #676

Human

Human Human Human

Aas24943 Aah83588 Aas25126

61 AGGAAATTGAAG 21 ATATACAACCGGG 21 ATATACAACCCGG 21 ATATACAACCCGG 81 GAGATAGAGATTA 81 GAGATAGAGATTA 81 CAACAAGCCAATC 1	TGTCGGTGCTATCTCCACCAGCAGGCCCGCGGAGCTCCCCCCGCTGCCCCTACCAC 126	0 8 4 4 0 0 6 6	1621 TCTTCCACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC	1861   AGCAAGTGCACCACAGCAAAACAACGGATGAATGTAGCCCTTCCAACAC
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XX XX XX Squence 3412 BP; 970 A; 887 C; 804 G; 750 T; 0 U; 1 Other;  Query Match Guery Match Guery Match Guery Match Guery Match Best Local Similarity 100.0%; Score 3412; DB 3; Length 3412; Best Local Similarity 100.0%; Pred. No. 0; Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 3412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  QY   GGCAGCGAGCAGCAGCAGCACCCGCCCGCCGCGCGCGCG	121 GACCTCCGGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTGAAG	Oy         301 AAGCTAAGGAGCAGGAAATTCGAAACTCCCTCCTCCTCCTCCTCGTGGGGGGTG 360           Db         301 AAGCTAAGGAGCAGAAAATTCGAACATCCTCTCTCTCTCT	541 GAAGAGGTGCCCTTCGCCCCTCAGCGGCCCCGGGGGGCCCTTCCCGG  [	84 84 90 96 96 110

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                             GIGITITITACCICAGCACCTTGCTCTTGTTTCCCTTAGAGATTTTGTAAAGCTGATAG
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(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC,

WPI; 2001-488783/53. P-PSDB; AAU16163.

New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives.

Claim 1; SEQ ID NO 329; 980pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to encoded secreted proteins. The nucleic acids and proteins are used to rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a alleviating symptoms associated with the disorders and in diagnostic alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune disease e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. corneal infection, are propertied and fungi and coular disorders e.g. corneal infection, and many other disorders e.g. Alzheimer's disease, infections caused by can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present the sequence encodes a novel secreted protein of the invention. Note: The

1988 AGATTANTGAAGAAGCTGCGTGAAGACTTTGAAAATGATATGCTGGCTG	Db   1951 AATGAGACCAAACGCAGCCAGGAGAGAAACCAAAGACCATCTGAGGAATGAG 2010
CC sequence data for this patent did not form part of the printed  Query Match  Best Local Similarity 9:04, pred, No. 0;  Bast Local Similarity 9:07, pred, No. 0;  Bast Concording Conformation Conformat	Db

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New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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29-SEP-2000; 2000US-0236370P.
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                                                                                                                                                          ROSEN C A.
RUBEN S M.
BARASH S C.
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P à 유 õ 셤 à ద õ 셤 à ద õ 뭐 à 셤 õ 셤 õ 검 The invention relates to human novel polypeptides and their associated polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rhematoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal bolyps and sinusitis), reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Bostein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. anomaly and hypoplastic left heart syndrome), renal disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. therosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent human novel polynucleotides of the invention 2 210 127 187 247 ACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCCATCGAGACCCTCTCGG 270 307 GGAGCAGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGGGTGTTGTTGTTGGATG 390 GGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTCC 150 GGAGCAGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTGTTGGATG 367 GCCAGCTCTTTGGGGACAGGAAGCTCCCCTGGCGGGACAGGTCCTGCTGAAGTCCGGCT GTAAAGTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAA GGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTCC GGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTGAAGTCCGGCT ACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCCATCCGCGCCATCGAGACCCTCTCGG Gaps ä; DB 7; Length 3694; 1; Indels Score 2953; DE Pred. No. 0; 0; Mismatches 86.5%; Query Match
Best Local Similarity 99.9
Matches 3303; Conservative 5 188 211 248 308 331 68 1.28 151 271

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<u>a</u> 2	691 728	TCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGGGTTGACCATAAAGAACATCA .
<b>3</b> 8	i in	CTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAAACTCTGGAGCTGCAGAGA
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<u>a</u>	⊣ :	AGCCIGICACCAICCACCCCCAGAGGGGACTICIGAAGCAIGCCGCAIGAITCITG
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>-	806	TGGCACACAATGGCTTGGTTGGAAGACTGGTTGGGAAAGAAGGCAGAAATTTGAAGAAAA
QQ	931	
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λ	1268	CTACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCGTTCCCGC 1327
q	1291	
λ	1328	ATCATCACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGG 1387
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>-	1388	GCGCCATCATCGGGAAGAAGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCT 14
Dp		GCGCCATCATCGGGAAGAAGAGGGGCACACATCAAACAGCTGGCGGAGATTCGCCGGAGCCT

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products for the diagnosis, monitoring and treatment of cancers.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food of sites expressing (II). (I) and (II) and (II) and (II) and (II) are useful for treating disorders polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and polymertic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                           and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at Electronic format directly from Lagrange at the wipo.int/pub/published_pct_sequences
                                                                                                                               ACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCGGTTCCCGGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a new method for assessing whether a patient is afflicted with ovarian cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where specification. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as possible, and the recurrence of ovarian cancer. The method may also be of particular use with patients having an enhanced risk of developing ovarian cancer (e.g. patients having a familial history of ovarian cancer). The cancer markers may be used in the management and treatment
                                                     3546 GGAGAAGGIGGACAGICCAAGIGTGCAACAGCIGITCTGAATIGICTTCCGCTAGCCAAGA 3605
                                                                                                                                                                                                                                                                                             Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meniagitis; viral meniagitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontubercrulous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
           TITITITITITITITIAATAAAATGAGTIGGAAAAAAAATAAGAIATCAACIGCCAGCCI
                                       GGAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAATTGTCTTCCGCTAGCCAAGA
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), Mills GB
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Sen A, Vieby PO,
, Glatt K;
                                                                                                                                                                                                                                                                       cDNA encoding human ovarian cancer marker M452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoersch S,
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RE, Zhao X,
                                                                                                                                                                                       ABS76442 standard; cDNA; 3667 BP
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10-MUG-2001; 2001US-0311732P.
19-SEP-2001; 2001US-032380P.
26-SEP-2001; 2001US-03254967P.
26-SEP-2001; 2001US-0325102P.
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Meyers RE, Morrisey MP, O
                                                                                                                                                                                                                                            (first entry)
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of e.g. brain and central nervous system disorders (e.g. bacterial and discase or parkinson's disease), brain disorders (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. cerebral oedema, hydrocephalus or brain herniations), inflammations (e.g. cerebral oedema, hydrocephalus or brain herniations), connective tissue disorders, or heart disorders (e.g. nontuberculous granulomatous orchitis), disease or atherosclerosis). The compositions and methods may also be used in assessing the histological type of neoplasm associated with evarian cancer, monitoring the progression of ovarian cancer, determining whether ovarian cancer has metastasized or is likely to metastasize, ovarian cancer has metastasized or is likely to metastasize, ovarian cancer arcinogenic potential of a compound, or inhibiting ovarian cancer arcinogenic potential of a compound, or inhibiting ovarian cancer or at risk of developing ovarian cancer. The present nucleic acid sequence encodes one of the ovarian cancer markers described in the
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Qy         3129 TAAATTCACAGATTTTTTAACGAGAAAAACACACAGAAGAAGATCCTCAGGTGTTTTT 3188           Db         3366 TAAATTCACAGATTTTTTTAACGAGAAAAACACACAGAGTGTTTTT 3425           Qy         3189 ACCTCAGCACCTTGTGTTTCCCTTAGAGATTTGTAAAGCTGATAGTTGGAGCA 3248           Db         3426 ACCTCAGCACCTTGTGTTTCCCTTAGAGATTTTGTAAAGCTGATAGTTGGAGCA 3485           Qy         3249 TTTTTTTTTTTTTTTTTTTATTAATAAAAATTGGAAAAATTAGTAAAGCTGATAGTTGGAGCA 3485           Db         3486 TTTTTTTTTTTTTTTTTTAATAAAAAATGAGTTGGAAAAAA	AAS26153 standard; CDNA, 2290 BP.  XX XX XX XX AAS26153, XX XX AAS26153, XX XX AAS26153, XX  Human; immunosuppressive; antiarthritic; se; antirheumatic; cytostatic; cardiant; vacotropic; neturoprotective; XX XX XX  Human; immunosuppressive; antiarthritic; se; antirheumatic; cytostatic; cardiant; vacotropic; neturoprotective; XX XX  Human; immunosuppressive; fungicide; optialandogical; vullnerary; XX  Cardiant; vacotropic; cardiac arreet; cerebrovascular disorder; XX  Alabelman; antipacterial; viluoide; fungicide; optialandogical; vullnerary; XX  XX  Mound healing; epithelial cell proliferation; skin ageing; fcod additive; XX XX XX XX XX XX XX XX XX XX XX XX XX	14-AUG-2000;
2050 GCGGGGAAGGTCAGCCAGGATTGCCAGAACCACCGAGCCCCCCCC	2350 ANTATATCANTACTCAACTACTCATTTTAATCAATTATTTTTTTT	

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21-SEP-2000; 2000US-0234937P.
25-SEP-2000; 2000US-0234997P.
26-SEP-2000; 2000US-0234997P.
27-SEP-2000; 2000US-0235834P.
27-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0235834P.
29-SEP-2000; 2000US-0235836P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236367P.
29-SEP-2000; 2000US-0236369P.
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(HUMA-) HUMAN GENOME SCI INC

Ruben SM; Barash SC, Rosen CA,

WPI; 2001-488783/53. P-PSDB; AAU16166.

and New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.

Claim 1; SEQ ID NO 332; 980pp; English.

The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a learn attaing symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune treoplasms of the breast or liver, cardiovascular disorders e.g. cheoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, becteria, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders listed in the specification. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, cramplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage

2347 AATAATATATCAAATAACTCAACTCCAATTTTTAATCAATTATT		2707 GITTARCCCCCCCCCCCCTCCCCTCCTCCTCCTCCTCCTCCTCCT	1356 G-TTATCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	2825 TCTGAGTATCACATCACAAAAGGAACAAAAGCGAAACACACAC	2885 CACTTGGTTA 	2945 AAACAGGAACCCACCAACCAATCAACCAAACAAAAAAAATTCCACAATGAAAG 3004 	3005 AATGIATITIGICITITIGGATITIGGIGIATAAGCCAICAATAITCAGCAAAAAGAITC 3 [	3065 CTTTCTTT-AP              1715 CTTTCTTTAAP	3124 GGCGTTAAATTCACAGATTTTTTTAACGAG 	3184 ITTTTACCTCAGCACCTTGCTCTTCCCTTAGAGATTTTGTAAAGCTGATAGTTG 3243 1835 ITTTTACCTCAGCACCTTGCTCTTTCCTTAGAGATTTTGTAAAGCTGATAGTTG 1894	3244 GAGCATTTTTTTTTTTTAATAAAATGAGTTGGAAAAAAAA	3304 AGCCTGGAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAATTGTCT 3354	RESULT 9 ABX73494 ID ABX73494 standard; DNA; 2290 BP. XX
8 8 8 8 8	8 8 8	3 8 8 8	da vo da	VQV Db	Å da	& A	% ଶ	& 8	λ α	У	oy Q	λό da	RESUI ABX73 ID XX
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  CC sequence encodes and other nutritional components. The present  CC sequence encodes a novel secreted protein of the invention. Note: The  CC sequence data for this patent did not form part of the printed  Query Match  Best Local Similarity 99.7%; Pred. No. 0;  Matches 1966; Conservative 0; Mismatches 1; Indels 4; Gaps 3;  QY 1387; GGGGCATCATGGGGAAGAAGGGGGCACACATCAAACAGGTGGCGAATTCGCGGAGCC 1446  DD 36, GGGCCATCATCGGAAAAAAGAGGGGGCACACATCAAACAGCTGGCGAATTCGCGGAACCCGGAGCC 1446  DD 36, GGGCCATCATCGGAAAAAAACAGGCGAAACAACATCAAACAGCTGGCGAACATCAACACATCAACATCAACAACAACAACAACAACAA	1447 TCTATCAAGATTGCCCTGCGGAAGGCCCAGACGAAGAAGGAAG	GGAACTGAAAG CCAGAGTGCCCTC              CCAGAGTGCCCTC	Db   276   ACAGCTGGCTGGTGTTTGGCAAAGGTGGCAAGACCGTGAACGAAC	1747 AGAATTATCGGGCACTTCTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTA 18	18 51	QY 1867 TGAGGCTCCCACAGCAAAACAACGGATGAATGTAGCCCTTCCAACACCTGACA 1926 		OY 1987 GAAGTCTGCGGAGGGGCCAGGGACTCTGCCGAGGACCCTGAGAACCCCAGGGGCCGAGGA 2046	QY       2047 GGGGGGGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGAGCCCGGCTCCGGCCCCCCCAG       2106         Db       696 GGGGGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGACCCCGCCTCCCGCCCCCCAG       755	QY 2107 GGCTTCTGCAGCTTCAGCCATCCACCATCCACTCGGATCTCTCTGAACTCCCA 2166	22	22 93	Oy 2287 AIGITAAGATATGTGGCCTGTGGGTTACACAGGGTGCCTGCAGCGGTAATATATTTAGA 2346

renal disorder;

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Human; gene; ds; neural disorder; immune system disorder; renal disorder muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; inflammatory disease; allergic reaction; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiatteriosclerotic.
                                                                                      Human novel polynucleotide #322.
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ABX73494;
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The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus exythematosus, rhemmatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. nasal bolyps and sinusitis), reproductive disorders, castrointestinal disorders, pulmonary disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left reart syndrome), renal disorders (e.g. acute kidney failure and en-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. asthma), blood related disorders (e.g. therosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent human novel polynucleotides of the invention 1506 1626 1686 1746 1806 1387 GGCGCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCC 1446 1507 GGGCCACCGGAAGCCCACTICAAGGCCCAGGACGGATCTITGGGAAACTGAAAGAGGAA 1566 395 455 215 275 95 New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular c TCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACC AGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTC 36 GCGCCATCATCGGGAAGAGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCC TCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACC GGGCCACCGGAAGCCCAGTTCAAGGCCCAGGACGGATCTTTGGGAAACTGAAAGAGAA 1567 AACTTCTTTAACCCCCAAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCC 216 AACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCC ACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGGAACTGCAGAACTTAACC <u> ACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGGAACTGCAGAACTTAACC</u> 1687 AGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTC 1747 AGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTA Gaps 4; Score 1496; DB 7; Length 2290; Pred. No. 0; Mismatches 1; Indels 4 Sequence 2290 BP; 707 A; 561 C; 491 G; 531 T; 0 U; 0 Other; Claim 1; SEQ ID NO 332; 402pp; English Barash SC; 43.8%; Matches 1966; Conservative Rosen CA, Ruben SM, WPI; 2003-147444/14 Local Similarity BARA/) BARASH S C. ROSEN C A. RUBEN S M. P-PSDB; ABU55234 renal disorders. 1447 96 156 1627 276 336 396 Query Match (ROSE/) Best à 엄 à g ð d ð g à g à 셤  $\overset{\sim}{\circ}$ g

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detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of premetastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
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cardiant, vasotropic, cerebroprotective, nootropic, neuroprotective,
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                                                                                                                                                                                                                                           Sequence 710 BP; 199 A; 174 C; 180 G; 152 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA encoding a novel secreted protein, Seq ID 749.
                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                           negative breast cancer, lung cancer, and colon cancer
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antibacterial; virucide; fungicide; opthalmalogical; vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
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                                2223 AATGCACACCCTTTTTCTGTGGCAAATCGTCTGTACATGTGTGTACATATTAGAAAGG
                                                                                                            2283 GAAGATGTTAAGATATGTGGCCTGTGGGTTACACAGGGTGCCTGCAGGGGTAATATTT
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28-JUN-2000; 2000US-018064P.
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14-AUG-2000; 2000US-0225267P.
14-AUG-2000; 2000US-0225267P.
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1924 ACAGAATGAGACCAAACGAGCCAGCCAGATCGGGAGCAAACCAAAGACCATCTGAGGAA 1983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1864 AAGTGAGGCTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGCCCTTCCAACACCTG 1923
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2000US-0229113P.
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572 ACAGAATGAGACCAAACGCAGCCAGATCGGGAGCAAACCAAAGACCATCTGAGGAA
                                    1984 TGAGAAGTCTGCGGAGGCGGCCAGGGACTCTGCCGAGGCCCTGAGAACCCCAGGGGCCGA
                                                       CAGGGCTTCTGCAGGCTTCAGCCAT-CCACTTCACCATCCACCTCGGATCTCTCCTGAACT
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                                                                                                         GGAGGGGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGAGCCCCGCCTCCCGCCCCC
                                                                                                                               692 GGAGGGGGGGAAAGTCAGCCAGGTTTGCCAGAACCACGAGCCCCGCCTCCCGCCCC
                                                                                                                                                                                                           CAGGGCTTCTGCAGGCTTCAGCNATNCCACTTCACCATCCACTCGGATCTCTCCTGAACT
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Claim 1; SEQ ID NO 330; 980pp; English.

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02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0239933P.
13-OCT-2000; 2000US-0239933P.
13-OCT-2000; 2000US-0239937P.
20-OCT-2000; 2000US-0241221P.
20-OCT-2000; 2000US-0241221P.
20-OCT-2000; 2000US-0241186P.
20-OCT-2000; 2000US-0241186P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-024647P.
08-NOV-2000; 2000US-024647P.
08-NOV-2000; 2000US-024647P.
08-NOV-2000; 2000US-024647P.
08-NOV-2000; 2000US-024647P.
08-NOV-2000; 2000US-0246528P.
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17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025188P.
06-DEC-2000; 2000US-025185P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
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prevent, treat or amellorate a medical condition in e.g. numans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a lead of pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ENISA) Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac nervous system disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, virtuses and fungi and ocular disorders e.g. corneal infection. Con also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, coffectors and other nutritional components. The present c sequence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
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BARASH S C. (ROSE/) ROSEN C A. (RUBE/) RUBEN S M. BARA/) 

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renal disorder;
            muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; hyperproliferative disorder; inflammatory disease; allergic reaction; blood related disorder; ancer; immunosuppressive; antififlammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; haemostatic; antiarteriosclerotic.
ds; neural disorder; immune system disorder;
                                                                                                                                                                                                                                                                                                                                             2000US-0216880P.
2000US-0217487P.
2000US-0217495P.
2000US-0218290P.
2000US-0220963P.
2000US-0220964P.
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2000US-0225477P
2000US-0225757P
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30-AUG-2000; 2000US-0228924P.
01-SEP-2000; 2000US-022934P.
01-SEP-2000; 2000US-0229343P.
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2000US-0237037P.
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2000US-0251869P
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14-AUG-2000; 2
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28-JUN-2000;
07-JUL-2000;
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11-JUL-2000; 2
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26-JUL-2000; 2
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02-OCT-2000; 2
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02-OCT-2000;
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14-AUG-2000;
                                                                                                                                      Homo sapiens
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14-AUG-2000;
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20-OCT-2000;
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01-NOV-2000;
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Barash SC:

Ruben SM,

Rosen CA,

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                                                                                                                                                                                        The invention relates to human novel polypeptides and their associated polymucleotides. The polypeptides and polymucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis and multiple sclerosis), muscular disorders, respiratory diseases (e.g. qastrointestinal disorders, pulmonary disorders, cardiovascular disorders, (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left heart syndrome), renal disorders (e.g. acute kidney failure and end-stage renal disease), hyperproliferative disorders (e.g. Hodgkin's disease and leukaemia,), inflammatory diseases (e.g. septic shock, bursitis and appendicitis), allergic reactions and conditions (e.g. stabma), blood related disorders (e.g. thrombosis, atherosclerosis and myocardial infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent
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                                                                  New polypeptides and nucleic acids, useful in gene therapy for treating, inhibiting or preventing e.g. neural, immune system, muscular, respiratory, reproductive, gastrointestinal, pulmonary, cardiovascular or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 389; DB 7;
Pred. No. 1.2e-163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       human novel polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                              Claim 1; SEQ ID NO 330; 402pp; English
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99.8%;
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                WPI; 2003-147444/14.
P-PSDB; ABU55232.
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                                                                                                                              renal disorders.
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Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 3265; 71pp + Sequence Listing; English.
        Human secreted protein 5' EST, SEQ ID NO: 3265.
                                                                                                                                                                     Duclert A,
                                                                                                              21-FEB-2000; 2000EP-00200610.
                                                                                                                                 99US-0122487P.
                                                                                                                                                                     Dumas Milne Edwards J,
                                                                                                                                                                                       WPI; 2000-500381/45
                                                                                                                                                                                                P-PSDB; AAG03261
                                                                                                                                                   (GEST ) GENSEI
                                                                         EP1033401-A2
                                                                                                                                 26-FEB-1999;
                                                                                           06-SEP-2000
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Giordano J;

The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. An ORP has been identified within the sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs and genomic 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, 198 CGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGGTAAAGT 257 258 GGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAGGAGCAG 317 GAACAAGCTTTACATCGGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTCCGGCAGCT 134 CTTTGGGGACAGGAAGCTGCCCCTGGCGGACAGGTCCTGCTGAAGTCCGGCTACGCCTT 194 138 criridegeacageaaecrecccreeceseacagerecrecrearereceseracecerr 197 CGTGGACTACCCCGACCAGAACTGGGCCATCGGCGCCATCGAGACCCTCTCGGGTAAAGT 254 GGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAGGAGCAG 314 GAACAAGCTTTACATCGGGAACCTGAGCCCGCCGTCACCGCCGACGACGACCTCCGGCAGCT 137 CGAGGAGCGCCGGGTACCGGGCCGGGGAGCCGCGGGCTCTCGGGGAAGAGGACGGTGAT 77 gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion CGAGGAGCGCCGGGTACCGGGCCCGGGGGCCCCCGGGGCTCTCGGGGAAGAGACGCATGAT Gaps . 0 315 GAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTGT 361 318 GAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTGT 364 10.2%; Score 347; DB 3; Length 364; 100.0%; Pred. No. 8.1e-145; Live 0; Mismatches 0; Indels Sequence 364 BP; 84 A; 101 C; 118 G; 59 T; 0 U; 2 Other; Query Match
Best Local Similarity 100.
Matches 347; Conservative 12 195 18 75 78 135 경 원 à q ò g 8 qq ð a

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